GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 14:57:02 ; Search time 534.27 Seconds
(without alignments)
12732.167 Million cell updates/sec

Title: US-08-153-397A-1
Perfect score: 3962
Sequence: 1 CGGGCCTGAGACTGGGGTGA.....AAAAAAAAAAACCGGAATTC 3962

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3962	100.0	3962	18	AAT93785	Human mammary carc
	2	3960.4	100.0	3962	16	AAQ92520	Human mammary carc
	3	3960.4	100.0	3962	16	AAQ92522	Human mammmary car
	4	3617.6	91.3	3754	16	AAQ84782	Protein-tyrosine-k
	5	3383.2	85.4	3554	24	AAS16842	Human epithelial d
	6	2783.6	70.3	2861	21	AAC99051	Human pancreatic c
	7	2783.6	70.3	2861	22	AAH33198	Human colon cancer
	8	642	16.2	3096	19	AAV48292	Discoidin domain r
	9	642	16.2	3157	16	AAQ92521	Human colonic aden
	10	642	16.2	3157	16	AAQ92523	Human colonic aden
	11	642	16.2	3157	18	AAT93784	CCK-2, a human mam
	12	639.8	16.1	3120	19	AAV55895	Receptor protein t
	13	639.8	16.1	3120	20	AAV65317	Receptor protein t
	14	544.2	13.7	2725	22	AAH99505	Human protein enco
c	15	522.8	13.2	563	23	AAS57829	cDNA #505 encoding
	16	453.4	11.4	2128	15	AAQ64158	Partial coding seq
	17	324.4	8.2	408	21	AAC00624	Human secreted pro
	18	236	6.0	272	16	AAT22477	Human gene signatu
c	19	228.4	5.8	463	22	ABA43008	Human breast cell
c	20	228.4	5.8	463	22	ABA53422	Human foetal liver
c	21	228.4	5.8	463	22	ABA23197	Probe #1663 for ge
c	22	228.4	5.8	463	22	AAK01693	Human brain expres
c	23	228.4	5.8	463	22	AAK27141	Human bone marrow
c	24	228.4	5.8	463	22	AAI11731	Probe #1664 for ge
c	25	228.4	5.8	463	22	AAI33038	Probe #1724 used t
c	26	228.4	5.8	463	22	AAI01659	Probe #1650 used t
	27	182.2	4.6	2820	16	AAT51456	gD.trkA fusion use
	28	180.6	4.6	1746	23	AAS84464	DNA encoding novel
	29	180.6	4.6	2301	19	AAV20445	Human c-trk oncoge
	30	180.6	4.6	2301	21	AAA09303	Human Trk oncogene
	31	180.6	4.6	3060	16	AAT51457	gD.trkB fusion use
	32	180.6	4.6	3194	16	AAT00689	Human trkB recepto
	33	180.6	4.6	3194	21	AAZ88839	Human trkB recepto
	34	180.6	4.6	3707	17	AAQ99277	Human neurotrophic
	35	180.2	4.5	2526	15	AAQ69029	Porcine TrkC gene.
	36	178.6	4.5	2526	13	AAQ28668	Encodes adult porc
	37	178.6	4.5	2526	14	AAQ34581	trkC clone in pFL1
	38	178.6	4.5	2940	16	AAT51458	gD.trkC fusion use
	39	177	4.5	2750	20	AAX87599	DNA coding for neu
	40	158	4.0	4092	20	AAV70230	Human receptor tyr
c	41	151	3.8	175	22	ABA48136	Human breast cell
c	42	151	3.8	175	22	ABA66013	Human foetal liver
c	43	151	3.8	175	22	ABA33099	Probe #11565 for g
c	44	151	3.8	175	22	AAK14437	Human brain expres
c	45	151	3.8	175	22	AAK40171	Human bone marrow

ALIGNMENTS

RESULT 1
AAT93785
ID AAT93785 standard; cDNA; 3962 BP.
XX
AC AAT93785;
XX
DT 16-FEB-1998 (first entry)
XX
DE Human mammary carcinoma kinase 10 (MCK-10) cDNA sequence.
XX
KW Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
KW proliferative disease; cancer; insulin receptor family;
KW tyrosine kinase neurotropin receptor; MCK-10 activity;
KW neurological disorder; aberrant expression; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 321..3077
FT /*tag= a
XX
PN US5677144-A.
XX
PD 14-OCT-1997.
XX
PF 08-NOV-1994; 94US-0336343.
XX
PR 16-NOV-1993; 93US-0153397.
XX
PA (ALVE/) ALVES F H E.
PA (ULLR/) ULLRICH A.
XX

PI Alves FHE, Ullrich A;
XX
DR WPI; 1997-511869/47.
DR P-PSDB; AAW34672.
XX
PT Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT for it, useful for cancer diagnosis
XX
PS Disclosure; Fig 1; 70pp; English.
XX
CC The present sequence represents the cDNA of a mammary carcinoma kinase,
CC called MCK-10. This kinase belongs to a novel family of receptor tyrosine
CC kinases, and expression is associated with proliferative diseases such as
CC cancer. The MCK-10 receptor tyrosine kinase has extensive sequence
CC similarity to the insulin receptor family. The MCK-10 gene was isolated
CC by PCR using 2 degenerate oligonucleotide primer pools, using a template
CC cDNA synthesised by reverse transcription of poly-A RNA from the human
CC mammary carcinoma cell line MCF7. MCK-10 is expressed in brain tissue,
CC and the protein shares homology with the tyrosine kinase neurotropin
CC receptor. Modulation of MCK-10 activity therefore may be used for
CC treatment of neurological disorders. MCK-10 is also expressed in a
CC variety of cancer cell lines and tumour tissue. The present sequence,
CC or parts of it, can be used for diagnostic purposes to detect aberrant
CC expression of MCK-10 genes. Inhibitors of MCK-10 receptor activity may
CC have therapeutic value in the treatment of diseases such as cancer.
XX
SQ Sequence 3962 BP; 735 A; 1234 C; 1182 G; 811 T; 0 other;

Query Match 100.0%; Score 3962; DB 18; Length 3962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 CCGGCTCCTGGCTCCCTCCGCCTCCCCCGCCCCTCGCCCCGCCGCCGAAGAGGCCCCGCT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     181 CCCGGGTCGGACGCCTGGGTCTGCCGGGAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT 240
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Db     181 cccgggtcggacgcctgggtctgccgggaagagcgatgagaggtgtctgaaggtggctat 240

Qy     241 TCACTGAGCGATGGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTA 300
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Qy     721 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 780
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Qy     841 TGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTT 900
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Qy  3541 AGGAGAGGAAAATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTC 3600
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Qy  3601 CTCCTCCATCACCTGAAACACTGGACCTGGGGGTAGCCCCGCCCCAGCCCTCAGTCACCC 3660
Db  3601 ctcctccatcacctgaaacactggacctgggggtagccccgccccagccctcagtcaccc 3660
Qy  3661 CCACTTCCCACTTGCAGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAG 3720
Db  3661 ccacttcccacttgcagtcttgtagctagaacttctctaagcctatacgtttctgtggag 3720
Qy  3721 TAAATATTGGGATTGGGGGGAAAGAGGGAGCAACGGCCCATAGCCTTGGGGTTGGACATC 3780
Db  3721 taaatattgggattgggggaaagagggagcaacggcccatagccttggggttggacatc 3780
Qy  3781 TCTAGTGTAGCTGCCACATTGATTTTTCTATAATCACTTGGGGTTTGTACATTTTTGGGG 3840
Db  3781 tctagtgtagctgccacattgatttttctataatcacttggggtttgtacatttttgggg 3840
Qy  3841 GGAGAGACACAGATTTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAATCCCCT 3900
Db  3841 ggagagacacagatttttacactaatatatggacctagcttgaggcaattttaatcccct 3900
```

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Qy   3901 GCACTAGGCAGGTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAAAAACCGGAAT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 gcactaggcaggtaataataaaggttgagttttccacaaaaaaaaaaaaaaaaaccggaat 3960

Qy   3961 TC 3962
          ||
Db   3961 tc 3962


RESULT   2
AAQ92520
ID   AAQ92520 standard; cDNA to mRNA; 3962 BP.
XX
AC   AAQ92520;
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human mammary carcinoma kinase 10 (MCK-10) cDNA.
XX
KW   Mammary carcinoma kinase 10; transmembrane receptor;
KW   receptor tyrosine kinase; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             321..3080
FT                   /*tag= a
FT   misc_difference 2315
FT                   /*tag= b
FT                   /note= "some clones have 6 AA deletion here"
XX
PN   WO9514088-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03797.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224054/29.
DR   P-PSDB; AAR75502.
XX
PT   New nucleic acid encoding MCK-10 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies useful
PT   for diagnosis and treatment of proliferative disease, esp. cancer,
PT   and for screening modulators
XX
PS   Claim 4; Page 50-52; 115pp; English.
XX
CC   cDNA prepd. from human breast cancer cell line MCF7 (ATCC HTB22) and
CC   used in a PCR with two degenerate oligo primer pools based on
CC   conserved sequences of the kinase domain of receptor tyrosine
CC   kinases. One clone, designated MCK-10, was identified as novel RTK.
CC   The PCR fragment was used to screen a lambda gt11 library of human
CC   fetal brain cDNA. Several overlapping clones were identified. The
CC   composite of these cDNA clones is given in AAQ92520 and the deduced AA
CC   sequence in AAR75502. Some of the clones had a deletion of 6 AAs at
CC   posn. 2315 in the MCK-10 sequence. MCK-10 has all the
CC   characteristics of a receptor PTK (see AAR75502 FT). Screening of
CC   human placental library yielded two cDNA clones MCK-10-1 and
CC   MCK-10-2. One of the clones isolated from the human fetal brain
CC   library contd. an additional 18 nts in the TK domain. The MCK-10 splice
CC   isoforms have been designated MCK-10-1 (with an additional 111 bp
CC   between nts 1832 and 1943); MCK-10-2 (without any insertions); MCK-10-3
CC   (with the additional 111 bp and and 18 bp in the TK domain); and MCK10-4
CC   (with the additional 18 bp). The predicted mol. wts. of MCK-10-1 and
CC   MCK-10-2 proreceptors are 101.13 and 97.17 kD respectively, and can thus
CC   be subdivided into a 34.31 kD alpha subunit and and 66.84 or 62.88 kD
CC   beta subunits that contain the TK homology and alternative splice sites.
XX
SQ   Sequence 3962 BP; 735 A; 1235 C; 1181 G; 811 T; 0 other;


  Query Match             100.0%;  Score 3960.4;  DB 16;  Length 3962;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3961;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CGGGCCTGAGACTGGGGTGACTGGGACCTAAGAGAATCCTGAGCTGGAGGCCCCCGACAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 cgggcctgagactggggtgactgggacctaagagaatcctgagctggaggcccccgacag 60

Qy      61 CTGCTCTCGGGAGCCGCCTCCCGACACCCGAGCCCCGCCGGCGCCTCCCGCTCCCGGCTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ctgctctcgggagccgcctcccgacacccgagccccgccggcgcctcccgctcccggctc 120

Qy     121 CCGGCTCCTGGCTCCCTCCGCCTCCCCCGCCCCTCGCCCCGCCGCCGAAGAGGCCCCGCT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ccggctcctggctccctccgcctccccgccccctcgccccgccgccgaagaggccccgct 180

Qy     181 CCCGGGTCGGACGCCTGGGTCTGCCGGGAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 cccgggtcggacgcctgggtctgccgggaagagcgatgagaggtgtctgaaggtggctat 240

Qy     241 TCACTGAGCGATGGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 tcactgagcgatggggttggacttgaaggaatgccaagagatgctgcccccacccccttа 300

Qy     301 GGCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ggcccgagggatcaggagctatgggaccagaggccctgtcatctttactgctgctgctct 360

Qy     361 TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 tggtggcaagtggagatgctgacatgaagggacattttgatcctgccaagtgccgctatg 420

Qy     421 CCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ccctgggcatgcaggaccggaccatcccagacagtgacatctctgcttccagctcctggt 480

Qy     481 CAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 cagattccactgccgcccgccacagcaggttggagagcagtgacggggatggggcctggt 540

Qy     541 GCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGAC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 gccccgcagggtcggtgtttcccaaggaggaggagtacttgcaggtggatctacaacgac 600

Qy     601 TCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 tccacctggtggctctggtgggcacccagggacggcatgccgggggcctgggcaaggagt 660

Qy     661 TCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCTGGATGGGCTGGAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 tctcccggagctaccggctgcgttactcccgggatggtcgccgctggatgggctggaagg 720

Qy     721 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 accgctggggtcaggaggtgatctcaggcaatgaggaccctgagggagtggtgctgaagg 780

Qy     781 ACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCCCGGGCTGACCGGGTCA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 accttgggcccccccatggttgcccgactggttcgcttctacccccgggctgaccgggtca 840

Qy     841 TGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 tgagtgtctgtctgcgggtagagctctatggctgcctctggagggatggactcctgtctt 900

Qy     901 ACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGGCCGTGTACCTCAACGACTCCA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 acaccgccccctgtggggcagacaatgtatttatctgaggccgtgtacctcaacgactcca 960
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Qy    961 CCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 cctatgacggacataccgtgggcggactgcagtatgggggtctgggccagctggcagatg 1020

Qy   1021 GTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 gtgtggtggggctggatgactttaggaagagtcaggagctgcgggtctggccaggctatg 1080

Qy   1081 ACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 actatgtgggatggagcaaccacagcttctccagtggctatgtggagatggagtttgagt 1140

Qy   1141 TTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ttgaccggctgagggccttccaggctatgcaggtccactgtaacaacatgcacacgctgg 1200

Qy   1201 GAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 gagcccgtctgcctggcggggtggaatgtcgcttccggcgtggccctgccatggcctggg 1260

Qy   1261 AGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 agggggagcccatgcgccacaacctaggggcaacctggggacccccagagcccgggctg 1320

Qy   1321 TCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 tctcagtgcccctggcggccgtgtggctcgctttctgcagtgccgcttcctctttgcgg 1380

Qy   1381 GGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggccctggttactcttcagcgaaatctccttcatctctgatgtggtgaacaattcctctc 1440

Qy   1441 CGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 cggcactgggaggcaccttcccgccagccccctggtggccgcctggcccacctcccacca 1500

Qy   1501 ACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGCCCGTGGCCAAGGCCGAGGGGA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 acttcagcagcttggagctggagcccagaggccagcagcccgtggccaaggccgagggga 1560

Qy   1561 GCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCATCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 gcccgaccgccatcctcatcggctgcctggtggccatcatcctgctcctgctgctcatca 1620

Qy   1621 TTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGAGGG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ttgccctcatgctctggcggctgcactggcgcaggctcctcagcaaggctgaacggaggg 1680

Qy   1681 TGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCAACA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 tgttggaagaggagctgacggttcacctctctgtccctggggacactatcctcatcaaca 1740

Qy   1741 ACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGCCCCGGCCTCGTGGGAATCCGC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 accgcccaggtcctagagagccacccccgtaccaggagccccggcctcgtgggaatccgc 1800

Qy   1801 CCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCTACC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 cccactccgctccctgtgtccccaatggctctgcgttgctgctctccaatccagcctacc 1860

Qy   1861 GCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCCCACACCCGCCT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 gcctccttctggccacttacgcccgtccccctcgaggcccgggcccccccacacccgcct 1920

Qy   1921 GGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 gggccaaacccaccaacacccaggcctacagtggggactatatggagcctgagaagccag 1980

Qy   1981 GCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCCCCCATTATGCCGAGGCTGACA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 gcgccccgcttctgccccacctccccagaacagcgtcccccattatgccgaggctgaca 2040

Qy   2041 TTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATGCTGTGCCTGCACTGCCCCCAG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ttgttaccctgcagggcgtcaccgggggcaacacctatgctgtgcctgcactgccccag 2100

Qy   2101 GGGCAGTCGGGGATGGGCCCCCCAGAGTGGATTTCCCTCGATCTCGACTCCGCTTCAAGG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 gggcagtcggggatgggccccccagagtggatttccctcgatctcgactccgcttcaagg 2160

Qy   2161 AGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAG 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 agaagcttggcgagggccagtttggggaggtgcacctgtgtgaggtcgacagccctcaac 2220

Qy   2221 ATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 atctggtcagtcttgatttcccccttaatgtgcgtaagggacacccttgctggtagctg 2280

Qy   2281 TCAAGATCTTACGGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTTCTCCAGGAATG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 tcaagatcttacggccagatgccaccaagaatgccagcttctccttgttctccaggaatg 2340

Qy   2341 ATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCCAACATCATTCGGCTGC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 atttcctgaaagaggtgaagatcatgtcgaggctcaaggaccccaacatcattcggctgc 2400

Qy   2401 TGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 tgggcgtgtgtgtgcaggacgacccccctctgcatgattactgactacatggagaacggcg 2460

Qy   2461 ACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 acctcaaccagttcctcagtgcccaccagctggaggacaaggcagccgagggggccccctg 2520

Qy   2521 GGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCTACCCAATGCTGCTGCATGTGGCAG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 gggacgggcaggctgcgcaggggcccaccatcagctacccaatgctgctgcatgtggcag 2580

Qy   2581 CCCAGATCGCCTCCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATCGGGACCTGG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 cccagatcgcctccggcatgcgctatctggccacactcaactttgtacatcgggacctgg 2640

Qy   2641 CCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCATCAAAATCGCAGACTTTGGCATGA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ccacgcggaactgcctagttggggaaaatttcaccatcaaaatcgcagactttggcatga 2700

Qy   2701 GCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGCCGGGCAGTGCTGCCCATCC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 gccggaacctctatgctggggactattaccgtgtgcagggccgggcagtgctgcccatcc 2760

Qy   2761 GCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGTGGG 2820
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Db   2761 gctggatggcctgggagtgcatcctcatggggaagttcacgactgcgagtgacgtgtggg 2820

Qy   2821 CCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTTGGGCAGC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 cctttggtgtgaccctgtgggaggtgctgatgctctgtagggcccagcccttgggcagc 2880

Qy   2881 TCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGTTCTTCCGGGACCAGGGCCGGCAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 tcaccgacgagcaggtcatcgagaacgcgggggagttcttccgggaccagggccggcagg 2940

Qy   2941 TGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCCTATATGAGCTGATGCTTCGGTGCT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 tgtacctgtcccggccgcctgcctgcccgcagggcctatatgagctgatgcttcggtgct 3000

Qy   3001 GGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCCAGCTGCATCGGTTCCTGGCAGAGG 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ggagccgggagtctgagcagcgaccacccttttcccagctgcatcggttcctggcagagg 3060

Qy   3061 ATGCACTCAACACGGTGTGAATCACACATCCAGCTGCCCCTCCCTCAGGGAGTGATCCAG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 atgcactcaacacggtgtgaatcacacatccagctgccctccctcagggagtgatccag 3120

Qy   3121 GGGAAGCCAGTGACACTAAAACAAGAGGACACAATGGCACCTCTGCCCTTCCCCTCCCGA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3121 gggaagccagtgacactaaaacaagaggacacaatggcacctctgcccttcccctcccga 3180

Qy   3181 CAGCCCATCACCTCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCACCCAGGGAG 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 cagcccatcacctctaatagaggcagtgagactgcaggtgggctgggcccacccagggag 3240

Qy   3241 CTGATGCCCCTTCTCCCCTTCCTGGACACACTCTCATGTCCCCTTCCTGTTCTTCCTTCC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 ctgatgcccctctcccctcctggacacactctcatgtcccctcctgttcttccttcc 3300

Qy   3301 TAGAAGCCCCTGTCGCCCACCCAGCTGGTCCTGTGGATGGGATCCTCTCCACCCTCCTCT 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 tagaagcccctgtcgcccacccagctggtcctgtggatgggatcctctccaccctcctct 3360

Qy   3361 AGCCATCCCTTGGGGAAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCCATTG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 agccatcccttggggaagggtggggagaaatataggatagacactggacatggcccattg 3420

Qy   3421 GAGCACCTGGGCCCCACTGGACAACACTGATTCCTGGAGAGGTGGCTGCGCCCCAGCTTC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 gagcacctgggccccactggacaacactgattcctggagaggtggctgcgccccagcttc 3480

Qy   3481 TCTCTCCCTGTCACACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGA 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 tctctccctgtcacacactggaccccactggctgagaatctgggggtgaggaggacaaga 3540

Qy   3541 AGGAGAGGAAAATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 aggagaggaaaatgtttccttgtgcctgctcctgtacttgtcctcagcttgggcttcttc 3600

Qy   3601 CTCCTCCATCACCTGAAACACTGGACCTGGGGGTAGCCCCGCCCCAGCCCTCAGTCACCC 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 ctcctccatcacctgaaacactggacctgggggtagccccgccccagccctcagtcaccc 3660

Qy   3661 CCACTTCCCACTTGCAGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAG 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 ccacttcccacttgcagtcttgtagctagaacttctctaagcctatacgtttctgtggag 3720

Qy   3721 TAAATATTGGGATTGGGGGGAAAGAGGGAGCAACGGCCCATAGCCTTGGGGTTGGACATC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 taaatattgggattgggggaaagagggagcaacggcccatagccttggggttggacatc 3780

Qy   3781 TCTAGTGTAGCTGCCACATTGATTTTTCTATAATCACTTGGGGTTTGTACATTTTTGGGG 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 tctagtgtagctgccacattgatttttctataatcacttggggtttgtacatttttgggg 3840

Qy   3841 GGAGAGACACAGATTTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAATCCCCT 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ggagagacacagatttttacactaatatatggacctagcttgaggcaattttaatccccT 3900

Qy   3901 GCACTAGGCAGGTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAAAAACCGGAAT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 gcactaggcaggtaataataaaggttgagttttccacaaaaaaaaaaaaaaaaaccggaat 3960

Qy   3961 TC 3962
          ||
Db   3961 tc 3962
```

```
RESULT   3
AAQ92522
ID   AAQ92522 standard; cDNA to mRNA; 3962 BP.
XX
AC   AAQ92522;
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human mammmary carcinoma kinase 10 (MCK-10) cDNA.
XX
KW   Mammary carcinoma kinase 10; MCK-10; transmembrane receptor;
KW   receptor tyrosine kinase; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             321..3080
FT                   /*tag= a
FT   misc_difference 2315
FT                   /*tag= b
FT                   /note= "some clones have AA deletion here"
XX
PN   WO9514089-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03799.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224055/29.
DR   P-PSDB; AAR75504.
XX
PT   New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies, useful
PT   for diagnosis and treatment of proliferative and nervous system
PT   diseases and for screening modulators
XX
PS   Disclosure; Page 67-69; 115pp; English.
XX
CC   cDNA prepd. from human breast cancer cell line MCF7 (ATCC HTB22) was
CC   used in a PCR with two degenerate oligo primer pools based on
CC   conserved sequences of the kinase domain of receptor tyrosine
CC   kinases. One clone, designated MCK-10, was identified as novle RTK.
CC   The PCR fragment was used to screen a lambda gt11 library of human
CC   fetal brain cDNA. Several overlapping clones were identified. The
CC   composite of these cDNA clones is given in AAQ92522 and the deduced AA
CC   sequence in AAR75504. Some of the clones had a deletion of 6AA at posn.
CC    2315 in the MCK-10 sequence. MCK-10 has all the characteristics of
CC   a receptor PTK (see AAR75504 FT). Screening of human placental library
CC   yielded two cDNA clones. One of the clones isolated from the human
CC   fetal brain library contained an additional 18 nts in the TK
CC   domain. The MCK-10 splice isoforms have been designated MCK-10-1
CC   (with an additional 111 bp between nts 1832 and 1943); MCK-10-2
CC   (without any insertions); MCK-10-3 (with the additional 111 bps and
CC   18 bp in the TK domain); and MCK-10-4 (with the additional 18 bp).
CC   The predicted mol. wts. of MCK-10-1 and MCK-10-2 proreceptors are
CC   101.13 and 97.17 kD respectively, and can thus be subdivided into a
CC   34.31 kD alpha subunit and a 66.84 or 62.88 kD beta subunits that
CC   contain the TK homology and alternative splice sites.
XX
SQ   Sequence 3962 BP; 735 A; 1235 C; 1181 G; 811 T; 0 other;
```

```
  Query Match           100.0%;  Score 3960.4;  DB 16;  Length 3962;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3961;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CGGGCCTGAGACTGGGGTGACTGGGACCTAAGAGAATCCTGAGCTGGAGGCCCCCGACAG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 cgggcctgagactggggtgactgggacctaagagaatcctgagctggaggcccccgacag 60

Qy      61 CTGCTCTCGGGAGCCGCCTCCCGACACCCGAGCCCCGCCGGCGCCTCCCGCTCCCGGCTC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ctgctctcgggagccgcctcccgacacccgagccccgccggcgcctcccgctcccggctc 120

Qy     121 CCGGCTCCTGGCTCCCTCCGCCTCCCCCGCCCCTCGCCCCGCCGCCGAAGAGGCCCCGCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ccggctcctggctccctccgcctcccccgccccctcgccccgccgccgaagaggccccgct 180

Qy     181 CCCGGGTCGGACGCCTGGGTCTGCCGGGAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 cccgggtcggacgcctgggtctgccgggaagagcgatgagaggtgtctgaaggtggctat 240
```

```
Qy    241 TCACTGAGCGATGGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tcactgagcgatggggttggacttgaaggaatgccaagagatgctgccccccacccccttta 300

Qy    301 GGCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ggcccgagggatcaggagctatgggaccagaggccctgtcatctttactgctgctgctct 360

Qy    361 TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 tggtggcaagtggagatgctgacatgaagggacattttgatcctgccaagtgccgctatg 420

Qy    421 CCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ccctgggcatgcaggaccggaccatcccagacagtgacatctctgcttccagctcctggt 480

Qy    481 CAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 cagattccactgccgcccgccacagcaggttggagagcagtgacggggatggggcctggt 540

Qy    541 GCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gccccgcagggtcggtgtttcccaaggaggaggagtacttgcaggtggatctacaacgac 600

Qy    601 TCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 tccacctggtggctctggtgggcacccagggacggcatgccgggggcctgggcaaggagt 660

Qy    661 TCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCTGGATGGGCTGGAAGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 tctcccggagctaccggctgcgttactcccgggatggtcgccgctggatgggctggaagg 720

Qy    721 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 accgctggggtcaggaggtgatctcaggcaatgaggaccctgagggagtggtgctgaagg 780

Qy    781 ACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCCCGGGCTGACCGGGTCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 accttgggcccccatggttgcccgactggttcgcttctaccccgggctgaccgggtca 840

Qy    841 TGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tgagtgtctgtctgcgggtagagctctatggctgcctctggagggatggactcctgtctt 900

Qy    901 ACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGGCCGTGTACCTCAACGACTCCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 acaccgcccctgtggggcagacaatgtatttatctgaggccgtgtacctcaacgactcca 960

Qy    961 CCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 cctatgacggacataccgtgggcggactgcagtatgggggtctgggccagctggcagatg 1020

Qy   1021 GTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 gtgtggtggggctggatgactttaggaagagtcaggagctgcgggtctggccaggctatg 1080

Qy   1081 ACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 actatgtgggatggagcaaccacagcttctccagtggctatgtggagatggagtttgagt 1140

Qy   1141 TTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ttgaccggctgagggccttccaggctatgcaggtccactgtaacaacatgcacacgctgg 1200

Qy   1201 GAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 gagcccgtctgcctggcggggtggaatgtcgcttccggcgtggccctgccatggcctggg 1260

Qy   1261 AGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 agggggagcccatgcgccacaacctagggggcaacctgggggaccccagagcccgggctg 1320

Qy   1321 TCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 tctcagtgcccctggcggccgtgtggctcgctttctgcagtgccgcttcctctttgcgg 1380

Qy   1381 GGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggccctggttactcttcagcgaaatctccttcatctctgatgtggtgaacaattcctctc 1440

Qy   1441 CGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 cggcactgggaggcaccttcccgccagccccctggtggccgcctggcccacctcccacca 1500

Qy   1501 ACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGCCCGTGGCCAAGGCCGAGGGGA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 acttcagcagcttggagctggagcccagaggccagcagcccgtggccaaggccgagggga 1560

Qy   1561 GCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCATCA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 gcccgaccgccatcctcatcggctgcctggtggccatcatcctgctcctgctgctcatca 1620

Qy   1621 TTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGAGGG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ttgccctcatgctctggcggctgcactggcgcaggctcctcagcaaggctgaacggaggg 1680

Qy   1681 TGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCAACA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 tgttggaagaggagctgacggttcacctctctgtccctggggacactatcctcatcaaca 1740

Qy   1741 ACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGCCCCGGCCTCGTGGGAATCCGC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 accgcccaggtcctagagagccaccccccgtaccaggagccccggcctcgtgggaatccgc 1800

Qy   1801 CCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCTACC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 cccactccgctccctgtgtccccaatggctctgcgttgctgctctccaatccagcctacc 1860

Qy   1861 GCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCCCCACACCCGCCT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 gcctccttctggccacttacgcccgtccccctcgaggcccgggcccccccacacccgcct 1920

Qy   1921 GGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGCCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 gggccaaacccaccaacacccaggcctacagtggggactatatggagcctgagaagccag 1980

Qy   1981 GCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCCCCCATTATGCCGAGGCTGACA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 gcgccccgcttctgccccacctccccagaacagcgtcccccattatgccgaggctgaca 2040

Qy   2041 TTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATGCTGTGCCTGCACTGCCCCCAG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ttgttaccctgcagggcgtcaccgggggcaacacctatgctgtgcctgcactgcccccag 2100

Qy   2101 GGGCAGTCGGGGATGGGCCCCCCAGAGTGGATTTCCCTCGATCTCGACTCCGCTTCAAGG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 gggcagtcggggatgggcccccccagagtggatttccctcgatctcgactccgcttcaagg 2160

Qy   2161 AGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAG 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 agaagcttggcgagggccagtttggggaggtgcacctgtgtgaggtcgacagccctcaac 2220

Qy   2221 ATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 atctggtcagtcttgatttcccccttaatgtgcgtaagggacacccttgctggtagctg 2280

Qy   2281 TCAAGATCTTACGGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTTCTCCAGGAATG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 tcaagatcttacggccagatgccaccaagaatgccagcttctccttgttctccaggaatg 2340

Qy   2341 ATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCCAACATCATTCGGCTGC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 atttcctgaaagaggtgaagatcatgtcgaggctcaaggaccccaacatcattcggctgc 2400

Qy   2401 TGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCG 2460
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```
Db   2401 tgggcgtgtgtgtgcaggacgacccccctctgcatgattactgactacatggagaacggcg 2460
Qy   2461 ACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTG 2520
Db   2461 acctcaaccagttcctcagtgcccaccagctggaggacaaggcagccgaggggggcccctg 2520
Qy   2521 GGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCTACCCAATGCTGCTGCATGTGGCAG 2580
Db   2521 gggacgggcaggctgcgcaggggcccaccatcagctacccaatgctgctgcatgtggcag 2580
Qy   2581 CCCAGATCGCCTCCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATCGGGACCTGG 2640
Db   2581 cccagatcgcctccggcatgcgctatctggccacactcaactttgtacatcgggacctgg 2640
Qy   2641 CCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCATCAAAATCGCAGACTTTGGCATGA 2700
Db   2641 ccacgcggaactgcctagttggggaaaatttcaccatcaaaatcgcagactttggcatga 2700
Qy   2701 GCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGCCGGGCAGTGCTGCCCATCC 2760
Db   2701 gccggaacctctatgctggggactattaccgtgtgcagggccgggcagtgctgcccatcc 2760
Qy   2761 GCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGTGGG 2820
Db   2761 gctggatggcctgggagtgcatcctcatggggaagttcacgactgcgagtgacgtgtggg 2820
Qy   2821 CCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTTGGGCAGC 2880
Db   2821 cctttggtgtgaccctgtgggaggtgctgatgctctgtagggcccagcccttgggcagc 2880
Qy   2881 TCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGTTCTTCCGGGACCAGGGCCGGCAGG 2940
Db   2881 tcaccgacgagcaggtcatcgagaacgcgggggagttcttccgggaccagggccggcagg 2940
Qy   2941 TGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCCTATATGAGCTGATGCTTCGGTGCT 3000
Db   2941 tgtacctgtcccggccgcctgcctgcccgcagggcctatatgagctgatgcttcggtgct 3000
Qy   3001 GGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCCAGCTGCATCGGTTCCTGGCAGAGG 3060
Db   3001 ggagccgggagtctgagcagcgaccacccttttcccagctgcatcggttcctggcagagg 3060
Qy   3061 ATGCACTCAACACGGTGTGAATCACACATCCAGCTGCCCCTCCCTCAGGGAGTGATCCAG 3120
Db   3061 atgcactcaacacggtgtgaatcacacatccagctgcccctccctcagggagtgatccag 3120
Qy   3121 GGGAAGCCAGTGACACTAAAACAAGAGGACACAATGGCACCTCTGCCCTTCCCCTCCCGA 3180
Db   3121 gggaagccagtgacactaaaacaagaggacacaatggcacctctgcccttccctcccga 3180
Qy   3181 CAGCCCATCACCTCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCACCCAGGGAG 3240
Db   3181 cagcccatcacctctaatagaggcagtgagactgcaggtgggctgggcccacccagggag 3240
Qy   3241 CTGATGCCCCTTCTCCCCTTCCTGGACACACTCTCATGTCCCCTTCCTGTTCTTCCTTCC 3300
Db   3241 ctgatgccccttctccccttcctggacacactctcatgtccccttcctgttcttccttcc 3300
Qy   3301 TAGAAGCCCCTGTCGCCCACCCAGCTGGTCCTGTGGATGGGATCCTCTCCACCCTCCTCT 3360
Db   3301 tagaagcccctgtcgcccacccagctggtcctgtggatgggatcctctccaccctcctct 3360
Qy   3361 AGCCATCCCTTGGGGAAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCCATTG 3420
Db   3361 agccatcccttggggaagggtggggagaaatataggatagacactggacatggcccattg 3420
Qy   3421 GAGCACCTGGGCCCCACTGGACAACACTGATTCCTGGAGAGGTGGCTGCGCCCCAGCTTC 3480
Db   3421 gagcacctgggccccactggacaacactgattcctggagaggtggctgcgccccagcttc 3480
Qy   3481 TCTCTCCCTGTCACACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGA 3540
Db   3481 tctctccctgtcacacactggaccccactggctgagaatctgggggtgaggaggacaaga 3540
Qy   3541 AGGAGAGGAAAATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTC 3600
Db   3541 aggagaggaaaatgtttccttgtgcctgctcctgtacttgtcctcagcttgggcttcttc 3600
Qy   3601 CTCCTCCATCACCTGAAACACTGGACCTGGGGGTAGCCCCGCCCCAGCCCTCAGTCACCC 3660
Db   3601 ctcctccatcacctgaaacactggacctgggggtagccccgccccagccctcagtcaccc 3660
Qy   3661 CCACTTCCCACTTGCAGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAG 3720
Db   3661 ccacttcccacttgcagtcttgtagctagaacttctctaagcctatacgtttctgtggag 3720
Qy   3721 TAAATATTGGGATTGGGGGGAAAGAGGGAGCAACGGCCCATAGCCTTGGGGTTGGACATC 3780
Db   3721 taaatattgggattgggggggaaagagggagcaacggcccatagccttggggttggacatc 3780
Qy   3781 TCTAGTGTAGCTGCCACATTGATTTTTCTATAATCACTTGGGGTTTGTACATTTTTGGGG 3840
Db   3781 tctagtgtagctgccacattgatttttctataatcacttggggtttgtacatttttgggg 3840
Qy   3841 GGAGAGACACAGATTTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAATCCCCT 3900
Db   3841 ggagagacacagattttacactaatatatggacctagcttgaggcaattttaatccccct 3900
Qy   3901 GCACTAGGCAGGTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAAAAACCGGAAT 3960
Db   3901 gcactaggcaggtaataataaaggttgagttttccacaaaaaaaaaaaaaaaaaccggaat 3960
Qy   3961 TC 3962
Db   3961 tc 3962
```

RESULT 4
AAQ84782
ID AAQ84782 standard; DNA; 3754 BP.
XX
AC AAQ84782;
XX
DT 17-AUG-1995 (first entry)
XX
DE Protein-tyrosine-kinase PTK22.
XX
KW Protein-tyrosine-kinase; PTK; discoidin domain receptor; cancer;
KW breast tumor; mamma carcinoma; diagnosis; prognosis; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 142..2886
FT /*tag= a
XX
PN WO9502187-A.
XX
PD 19-JAN-1995.
XX
PF 08-JUL-1994; 94WO-GB01480.
XX
PR 09-JUL-1993; 93GB-0014271.
XX
PA (CANC-) CANCER RES INST.
PA (WELL) WELLCOME FOUND LTD.
XX
PI Barker KT, Crompton MR, Gusterson BA, Martindale JE;
PI Mitchell PJ, Page MJ, Spence P;
XX
DR WPI; 1995-066991/09.
DR P-PSDB; AAR71100.
XX
PT Method for screening substances, using protein tyrosine kinase -
PT for potential utility as therapeutic agents for cancer

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XX
PS   Claim 1; Page 26-30; 51pp; English.
XX
CC   cDNA derived from tumor metastatic tissue was amplified using
CC   primers (given in AAQ84783-84) based on sequences (AAR71101, AAR71103)
CC   associated with protein-tyrosine-kinases (PTK).  Novel PTK22 was
CC   identified in an isolated subclone.  The 3' sequence of PTK22 was
CC   obtained by reverse transcription (using the primer of AAQ84786) and
CC   PCR amplification (primers AAQ84787-88) of RNA of human breast
CC   carcinoma cell line MDA MG 468.  The partial DNA sequence of PTK22
CC   is given in AAQ84782.
XX
SQ   Sequence 3754 BP; 713 A; 1145 C; 1121 G; 775 T; 0 other;

  Query Match             91.3%;  Score 3617.6;  DB 16;  Length 3754;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 3728;  Conservative    0;  Mismatches   19;  Indels   29;  Gaps    7;

Qy    181 CCCGGGTCGGACGCCTGGGTCTGCCGGGAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT 240
          || ||   | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ccgggtcggaccgcctgggtctgccgggaagagcgatgagaggtgtctgaaggtggctat 61

Qy    241 TCACTGAGCGATGGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 tcactgagcgatggggttggacttgaaggaatgccaagagatgctgccccccacccccttа 121

Qy    301 GGCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 ggcccgagggatcaggagctatgggaccagaggccctgtcatctttactgctgctgctct 181

Qy    361 TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 tggtggcaagtggagatgctgacatgaagggacattttgatcctgccaagtgccgctatg 241

Qy    421 CCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 ccctgggcatgcaggaccggaccatcccagacagtgacatctctgcttccagctcctggt 301

Qy    481 CAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 cagattccactgccgcccgccacagcaggttggagagcagtgacggggatggggcctggt 361

Qy    541 GCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 gccccgcagggtcggtgtttcccaaggaggaggagtacttgcaggtggatctacaacgac 421

Qy    601 TCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 tccacctggtggctctggtgggcacccagggacggcatgccgggggcctgggcaaggagt 481

Qy    661 TCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCTGGATGGGCTGGAAGG 720
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    482 tctcccggagctaccggctgcgttactcccggcatggtcgccgctggatgggctggaagg 541

Qy    721 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 780
          |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 accgctgggtgcaggaggtgatctcaggcaatgaggaccctgagggagtggtgctgaagg 601

Qy    781 ACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCCCGGGCTGACCGGGTCA 840
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    602 accttgggccccccatggttgcccgactggttcgcttgtaccccgggctgaccgggtca 661

Qy    841 TGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTT 900
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    662 tgagcgtctgtctgcgggtagagctctatggctgcctctggagggatggactcctgtatt 721

Qy    901 ACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGGCCGTGTACCTCAACGACTCCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 acaccgcccctgtggggcagacaatgtatttatctgaggccgtgtacctcaacgactcca 781

Qy    961 CCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    782 cctatgacggacataccgtgggcggactgcagtatgggggtctgggccagctggcagatg 841

Qy   1021 GTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    842 gtgtggtggggctggatgactttaggaagagtcaggagctgcgggtctggccaggctatg 901

Qy   1081 ACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    902 actatgtgggatggagcaaccacagcttctccagtggctatgtggagatggagtttgagt 961

Qy   1141 TTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    962 ttgaccggctgagggccttccaggctatgcaggtccactgtaacaacatgcacacgctgg 1021

Qy   1201 GAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1022 gagcccgtctgcctggcggggtggaatgtcgcttccggcgtggccctgccatggcctggg 1081

Qy   1261 AGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1082 aggggagcccatgcgccacaacctagggggcaacctgggggaccccagagcccgggctg 1141

Qy   1321 TCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1142 tctcagtgcccttggcggccgtgtggctcgctttctgcagtgccgcttcctctttgcgg 1201

Qy   1381 GGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 ggccctggttactcttcagcgaaatctccttcatctctgatgtggtgaacaattcctctc 1261

Qy   1441 CGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 cggcactgggaggcaccttcccgccagccccctggtggccgcctggcccacctcccacca 1321

Qy   1501 ACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGC---AGCCCGTGGCCAAGGCCGAGG 1557
          |||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db   1322 acttcagcagcttggagctggagcccagaggccagccaaggcccgtggccaaggccgagg 1381

Qy   1558 GGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCA 1617
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Db   1382 ggagcccgaccgccatcctcatcggctgcctggtggccatcatcctgctcctgctgctca 1441

Qy   1618 TCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGA 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 tcattgccctcatgctctggcggctgcactggcgcaggctcctcagcaaggctgaacgga 1501

Qy   1678 GGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCA 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1502 gggtgttggaagaggagctgacggttcacctctctgtccctggggacactatcctcatca 1561

Qy   1738 ACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGCCCCGGCCTCGTGGGAATC 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1562 acaaccgcccaggtcctagagagccaccccgtaccaggagccccggcctcgtgggaatc 1621

Qy   1798 CGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCT 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1622 cgccccactccgctccctgtgtccccaatggctctgcgttgctgctctccaatccagcct 1681

Qy   1858 ACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCCCACACCCG 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682 accgcctccttctggccacttacgcccgtcccctcgaggcccgggcccccccacacccg 1741

Qy   1918 CCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGC 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1742 cctgggccaaacccaccaacacccaggcctacagtggggactatatggagcctgagaagc 1801

Qy   1978 CAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCCCCCATTATGCCGAGGCTG 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1802 caggcgccccgcttctgcccccacctccccagaacagcgtccccccattatgccgaggctg 1861

Qy   2038 ACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATGCTGTGCCTGCACTGCCCC 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1862 acattgttaccctgcagggcgtcaccgggggcaacacctatgctgtgcctgcactgcccc 1921
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Qy   2098 CAGGGGCAGTCGGGGATGGGCCCCCCAGAGTGGATTTCCCTCGATCTCGACTCCGCTTCA 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1922 cagggcagtcgggatgggccccccagagtggatttccctcgatctcgactccgcttca 1981

Qy   2158 AGGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTC 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1982 aggagaagcttggcgagggccagtttggggaggtgcacctgtgtgaggtcgacagccctc 2041

Qy   2218 AAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAG 2277
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
pb   2042 aagatctggttagtcttgatttcccccttaatgtgcgtaagggacacccttt gctggtag 2101

Qy   2278 CTGTCAAGATCTTACGGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTTCTCCAGGA 2337
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2102 ctgtcaagatcttacggccagatgccaccaagaatg----------ccagga 2143

Qy   2338 ATGATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCCAACATCATTCGGC 2397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 atgatttcctgaaagaggtgaagatcatgtcgaggctcaaggacccaaacatcattcggc 2203

Qy   2398 TGCTGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACG 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2204 tgctgggcgtgtgtgtgcaggacgacccccctctgcatgattactgactacatggagaacg 2263

Qy   2458 GCGACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCC 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2264 gcgacctcaaccagttcctcagtgcccaccagctggaggacaaggcagccgaggggccc 2323

Qy   2518 CTGGGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCTACCCAATGCTGCTGCATGTGG 2577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324 ctggggacgggcaggctgcgcaggggcccaccatcagctacccaatgctgctgcatgtgg 2383

Qy   2578 CAGCCCAGATCGCCTCCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATCGGGACC 2637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384 cagcccagatcgcctccggcatgcgctatctggccacactcaactttgtacatcgggacc 2443

Qy   2638 TGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCATCAAAATCGCAGACTTTGGCA 2697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444 tggccacgcggaactgcctagttggggaaaatttcaccatcaaaatcgcagactttggca 2503

Qy   2698 TGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGCCGGGCAGTGCTGCCCA 2757
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Db   2504 tgagccggaacctctatgctggggactattaccgtgtgcagggccgggcagtgctgccca 2563

Qy   2758 TCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGT 2817
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Db   2564 tccgctggatggcctgggagtgcatcctcatggggaagttcacgactgcgagtgacgtgt 2623

Qy   2818 GGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTTGGGC 2877
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Db   2624 gggcctttggtgtgaccctgtgggaggtgctgatgctctgtagggcccagcccttgggc 2683

Qy   2878 AGCTCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGTTCTTCCGGGACCAGGGCCGGC 2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2684 agctcaccgacgagcaggtcatcgagaacgcgggggagttcttccgggaccagggccggc 2743

Qy   2938 AGGTGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCCTATATGAGCTGATGCTTCGGT 2997
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Db   2744 aggtgtacctgtcccggccgcctgcctgcccgcagggcctatatgagctgatgcttcggt 2803

Qy   2998 GCTGGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCCAGCTGCATCGGTTCCTGGCAG 3057
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Qy   3058 AGGATGCACTCAACACGGTGTGAATCACACATCCAGCTGCCCCTCCCTCAGGGAGTGATC 3117
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Db   2864 aggatgcactcaacacggtgtgaatcacacatccagctgcccctccctcagggagcgatc 2923

Qy   3118 CAGGGGAAGCCAGTGACACTAAAACAAGAGGACACAATGGCACCTCTG-CCCTTCCCCTC 3176
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2924 caggggaagccagtgacactaaaacaagaggacacaatggcacctctgcccctccctc 2983

Qy   3177 CCGACAGCCCATCACCTCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCACCCAG 3236
          |||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db   2984 ccgacagcccatcacctctaatagaggcagtgagactgca----ggctgggcccacccag 3039

Qy   3237 GGAGCTGATGCCCCTTCTCCCCTTCCTGGACACACTCTCATGTCCCCTTCCTGTTCTTCC 3296
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Db   3040 ggagctgatgccccttctcccctttcctggacacactctcatgtcccctttcctgttcttcc 3099

Qy   3297 TTCCTAGAAGCCCCTGTCGCCCACCCAGCTGGTCCTGTGGATGGGATCCTCTCCACCCTC 3356
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Db   3100 ttcctagaagcccctgtcgcccacccagctggtcctgtggatgggatcctctccacccac 3159

Qy   3357 CTCTAGCCATCCCTTGGGGAAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCC 3416
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Qy   3417 ATTGGAGCACCTGGGCCCCACTGGACAACACTGATTCCTGGAGAGGTGGCTGCG-CCCCA 3475
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Qy   3476 GCTTCTCTCTCCCTGTCACACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGA 3535
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Qy   3536 CAAGAAGGAGAGGAAAATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCT 3595
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Db   3340 caagaaggagaggaaaatgtttccttgtgcctgctcctgtacttgtcctcagcttgggct 3399

Qy   3596 TCTTCCTCCTCCATCACCTGAAACACTGGACCTGGGGGTAGCCCCGCCCCAGCCCTCAGT 3655
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Qy   3656 CA-CCCCCACTTCCCACTTGCAGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCT 3714
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Qy   3715 GTGGAGTAAATATTGGGATTGGGGGGAAAGAGGGAGCAACGGCCCATAGCCTTGGGGTTG 3774
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Qy   3775 GACATCTCTAGTGTAGCTGCCACATTGATTTTTCTATAATCACTTGGGGTTTGTACATTT 3834
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   3580 gacatctctagtgtagctgccacattgatttttctataatcactt-gggtttgtacattt 3638

Qy   3835 TTGGGGGGAGAGACACAGATTTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAA 3894
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Qy   3895 TCCCCTGCACTAGGCAGGTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAA 3950
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Db   3699 tcccctgcactaggcaggtaataataaaggttgagttttccacaaaaaaaaaaaaaa 3754
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RESULT   5
AAS16842
ID   AAS16842 standard; cDNA; 3554 BP.
XX
AC   AAS16842;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human epithelial discoidin domain receptor 1 (YSG5) trkE cDNA.
XX
KW   YSG; YSG5; schizophrenia; chronic animal model; LCGU; netrin receptor;
KW   local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
KW   calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;
KW   epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;
KW   tumour necrosis factor alpha; TNF-alpha; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             46..2676
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FT                   /*tag= a
FT                   /product= "Human trkE polypeptide"
XX
PN   WO200175440-A2.
XX
PD   11-OCT-2001.
XX
PF   02-APR-2001; 2001WO-GB01486.
XX
PR   31-MAR-2000; 2000GB-0007880.
PR   26-MAY-2000; 2000GB-0012768.
XX
PA   (WELF-) WELFIDE CORP.
XX
PI   Cochran S,  Paterson G,  Ohashi Y,  Morris B,  Pratt J;
XX
DR   WPI; 2002-010813/01.
DR   P-PSDB; AAU10542.
XX
PT   Novel chronic animal model of schizophrenia, useful for identifying
PT   anti-psychotic drugs and genes that are associated with schizophrenia
PT   -
XX
PS   Claim 1; Fig 7a; 79pp; English.
XX
CC   The invention relates to YSG polynucleotide fragments for use in
CC   diagnosing and/or developing treatments for schizophrenia using chronic
CC   animal models. The polynucleotides and their encoded polypeptides are
CC   used for identification of compounds which modulate the expression of YSG
CC   molecules, leading to the manufacture of schizophrenia medicaments. The
CC   sequences can also be used for testing candidate compounds for any effect
CC   on the polypeptides. Anti-schizophrenic effects of a compound can be
CC   determined by measuring local cerebral glucose utilisation (LCGU) or
CC   comparing its expression level with that of a control group. The
CC   sequences are useful in the identification of genes associated with
CC   schizophrenic states and in the development of an antibody. The sequences
CC   of the invention include phosphodiesterase 1-alpha, calcium-independent
CC   alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain
CC   receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and
CC   tumour necrosis factor (TNF) alpha. This sequence represents human
CC   epithelial discoidin domain receptor 1, trkE (YSG5) DNA.
XX
SQ   Sequence 3554 BP; 682 A; 1064 C; 1065 G; 743 T; 0 other;
```

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  Query Match           85.4%;  Score 3383.2;  DB 24;  Length 3554;
  Best Local Similarity  96.4%;  Pred. No. 0;
  Matches 3545;  Conservative    0;  Mismatches    3;  Indels  130;  Gaps    3;

Qy    277 AGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCC 336
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Db      2 agagatgctgcccccaccccctttaggcccgagggatcaggagctatgggaccagaggccc 61

Qy    337 TGTCATCTTTACTGCTGCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGACATT 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 tgtcatctttactgctgctgctcttggtggcaagtggagatgctgacatgaagggacatt 121

Qy    397 TTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTG 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 ttgatcctgccaagtgccgctatgccctgggcatgcaggaccggaccatcccagacagtg 181

Qy    457 ACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGA 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 acatctctgcttccagctcctggtcagattccactgccgcccgccacagcaggttggaga 241

Qy    517 GCAGTGACGGGGATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGT 576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 gcagtgacggggatggggcctggtgccccgcagggtcggtgtttcccaaggaggaggagt 301

Qy    577 ACTTGCAGGTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGC 636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 acttgcaggtggatctacaacgactccacctggtggctctggtgggcacccagggacggc 361

Qy    637 ATGCCGGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATG 696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 atgccgggggcctgggcaaggagttctcccggagctaccggctgcgttactcccgggatg 421

Qy    697 GTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGG 756
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Db    422 gtcgccgctggatgggctggaaggaccgctggggtcaggaggtgatctcaggcaatgagg 481

Qy    757 ACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCT 816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 accctgagggagtggtgctgaaggaccttgggcccccccatggttgcccgactggttcgct 541

Qy    817 TCTACCCCCGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCC 876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 tctaccccgggctgaccgggtcatgagtgtctgtctgcgggtagagctctatggctgcc 601

Qy    877 TCTGGAGGGATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTG 936
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Db    602 tctggagggatggactcctgtcttacaccgccccctgtggggcagacaatgtatttatctg 661

Qy    937 AGGCCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATG 996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 aggccgtgtacctcaacgactccacctatgacggacataccgtgggcggactgcagtatg 721

Qy    997 GGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGG 1056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 ggggtctgggccagctggcagatggtgtggtggggctggatgactttaggaagagtcagg 781

Qy   1057 AGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTG 1116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    782 agctgcgggtctggccaggctatgactatgtgggatggagcaaccacagcttctccagtg 841

Qy   1117 GCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCC 1176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    842 gctatgtggagatggagtttgagtttgaccggctgagggccttccaggctatgcaggtcc 901

Qy   1177 ACTGTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCC 1236
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Db    902 actgtaacaacatgcacacgctgggagcccgtctgcctggcggggtggaatgtcgcttcc 961

Qy   1237 GGCGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACC 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    962 ggcgtggccctgccatggcctgggaggggggagcccatgcgccacaacctaggggggcaacc 1021

Qy   1297 TGGGGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTC 1356
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Db   1022 tgggggaccccagagcccgggctgtctcagtgccccttggcggccgtgtggctcgctttc 1081

Qy   1357 TGCAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCT 1416
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Db   1082 tgcagtgccgcttcctctttgcggggccctggttactcttcagcgaaatctccttcatct 1141

Qy   1417 CTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGT 1476
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Db   1142 ctgatgtggtgaacaattcctctccggcactgggaggcaccttcccgccagcccccTggt 1201

Qy   1477 GGCCGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGC 1536
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Qy   1537 AGCCCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCA 1596
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Qy   1597 TCATCCTGCTCCTGCTGCTCATCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGC 1656
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Qy   1657 TCCTCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCC 1716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382 tcctcagcaaggctgaacggagggtgttggaagaggagctgacggttcacctctctgtcc 1441

Qy   1717 CTGGGGACACTATCCTCATCAACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGG 1776
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Db  1442 ctggggacactatcctcatcaacaaccgcccaggtcctagagagccacccccgtaccagg 1501
Qy  1777 AGCCCCGGCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGT 1836
Db  1502 agccccggcctcgtgggaatccgccccactccgctccctgtgtccccaatggctct---- 1557
Qy  1837 TGCTGCTCTCCAATCCAGCCTACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAG 1896
Db  1558 ------------------------------------------------------------ 1557
Qy  1897 GCCCGGGCCCCCCCACACCCGCCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGGG 1956
Db  1558 ----------------------------------------------gcctacagtgggg 1570
Qy  1957 ACTATATGGAGCCTGAGAAGCCAGCGCCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCG 2016
Db  1571 actatatggagcctgagaagccaggcgccccgcttctgcccccacctccccagaacagcg 1630
Qy  2017 TCCCCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCT 2076
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Qy  2077 ATGCTGTGCCTGCACTGCCCCCAGGGGCAGTCGGGGATGGGCCCCCCAGAGTGGATTTCC 2136
Db  1691 atgctgtgcctgcactgcccccaggggcagtcggggatgggcccccagagtggatttcc 1750
Qy  2137 CTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACC 2196
Db  1751 ctcgatctcgactccgcttcaaggagaagcttggcgagggccagtttggggaggtgcacc 1810
Qy  2197 TGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTA 2256
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Qy  2437 TTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGG 2496
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Db  2153 acccaatgctgctgcatgtggcagcccagatcgcctccggcatgcgctatctagccacac 2212
Qy  2617 TCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCA 2676
Db  2213 tcaactttgtacatcgggacctggccacgcggaactgcctagttggggaaaatttcacca 2272
Qy  2677 TCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTGC 2736
Db  2273 tcaaaatcgcagactttggcatgagccggaacctctatgctggggactattaccgtgtgc 2332
Qy  2737 AGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGT 2796
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Qy  2797 TCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCT 2856
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Qy  3097 CCCCTCCCTCAGGGAGTGATCCAGGGGAAGCCAGTGACACTAAAACAAGAGGACACAATG 3156
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Qy  3217 GGTGGGCTGGGCCCACCCAGGGAGCTGATGCCCCTTCTCCCCTTCCTGGACACACTCTCA 3276
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Qy  3397 ATAGACACTGGACATGGCCCATTGGAGCACCTGGGCCCCACTGGACAACACTGATTCCTG 3456
Db  2993 atagacactggacatggcccattggagcacctgggccccactggacaacactgattcctg 3052
Qy  3457 GAGAGGTGGCTGCG-CCCCAGCTTCTCTCTCCCTGTCACACACTGGACCCCACTGGCTGA 3515
Db  3053 gagaggtggctgcgccccccagcttctctctccctgtcacacactggaccccactggctga 3112
Qy  3516 GAATCTGGGGGTGAGGAGGACAAGAAGGAGAGGAAAATGTTTCCTTGTGCCTGCTCCTGT 3575
Db  3113 gaatctgggggtgaggaggacaagaaggagaggaaaatgtttccttgtgcctgctcctgt 3172
Qy  3576 ACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCACCTGAAACACTGGACCTGGGGGTA 3635
Db  3173 acttgtcctcagcttgggcttcttcctcctccatcacctgaaacactggacctggggta 3232
Qy  3636 GCCCCGCCCCAGCCCTCAGTCACCCCCACTTCCCACTTGCAGTCTTGTAGCTAGAACTTC 3695
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Qy  3696 TCTAAGCCTATACGTTTCTGTGGAGTAAATATTGGGATTGGGGGGAAAGAGGGAGCAACG 3755
Db  3293 tctaagcctatacgtttctgtggagtaaatattgggattgggggaaagagggagcaacg 3352
Qy  3756 GCCCATAGCCTTGGGGTTGGACATCTCTAGTGTAGCTGCCACATTGATTTTTCTATAATC 3815
Db  3353 gcccatagccttggggttggacatctctagtgtagctgccacattgatttttctataatc 3412
Qy  3816 ACTTGGGGTTTGTACATTTTTGGGGGGAGAGACACAGATTTTTACACTAATATATGGACC 3875
Db  3413 acttggggtttgtacatttttgggggagagacacagattttacactaatatatggacc 3472
Qy  3876 TAGCTTGAGGCAATTTTAATCCCCTGCACTAGGCAGGTAATAATAAAGGTTGAGTTTTCC 3935
Db  3473 tagcttgaggcaattttaatcccctgcactaggcaggtaataataaaggttgagttttcc 3532
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Qy   3936 ACAAAAAAAAAAAAAAA 3953
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Db   3533 acaaaaaaaaaaaaaaa 3550
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RESULT 6
AAC99051
ID AAC99051 standard; cDNA; 2861 BP.
XX
AC AAC99051;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:279.
XX
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic;
KW neural; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative; ss.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05989.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-579444/54.
DR P-PSDB; AAB54286.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
PS Claim 1; Page 714-715; 1379pp; English.
XX
CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 2861 BP; 567 A; 899 C; 800 G; 589 T; 6 other;

Query Match 70.3%; Score 2783.6; DB 21; Length 2861;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2833; Conservative 5; Mismatches 4; Indels 20; Gaps 3;

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Qy   1093 GGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGA 1152
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Db      1 ggcacarccacagcttctccagtggctatgtggagatggagtttgagtttgaccggctga 60

Qy   1153 GGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGGGAGCCCGTCTGC 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gggccttccaggctatgcaggtccactgtaacaacatgcacacgctgggagcccgtctgc 120

Qy   1213 CTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCA 1272
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Db    121 ctggcggggtggaatgtcgcttccggcgtggccctgccatggcctgggaggggggagccca 180

Qy   1273 TGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCC 1332
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Qy   1333 TTGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTAC 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1393 TCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAG 1452
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Qy   1453 GCACCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCAACTTCAGCAGCT 1512
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Qy   1513 TGGAGCTGGAGCCCAGAGGCCAGCAGCCCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCA 1572
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Qy   1573 TCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCATCATTGCCCTCATGC 1632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1633 TCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGG 1692
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Qy   1693 AGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCAACAACCGCCCAGGTC 1752
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Qy   1753 CTAGAGAGCCACCCCCGTACCAGGAGCCCCGGCCTCGTGGGAATCCGCCCCACTCCGCTC 1812
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Db    661 ctagagagccaccccgtaccaggagccccggcctcgtgggaatccgccccactcygctc 720

Qy   1813 CCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCTACCGCCTCCTTCTGG 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 cctgtgtccccaatggctctgcgttgctgctctccaatccagcctaccgcctccttctgg 780

Qy   1873 CCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCCCACACCCGCCTGGGCCAAACCCA 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ccacttacgcccgtcccccтcgaggcccgggcccccccacacccgcctgggccaaaccca 840

Qy   1933 CCAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTC 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ccaacacccaggcctacagtggggactatatggagcctgagaagccaggcgccccgcttc 900

Qy   1993 TGCCCCCACCTCCCCAGAACAGCGTCCCCCATTATGCCGAGGCTGACATTGTTACCCTGC 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2053 AGGGCGTCACCGGGGGCAACACCTATGCTGTGCCTGCACTGCCCCCAGGGGCAGTCGGGG 2112
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Db    961 agggcgtcaccgggggcaacacctatgctgtgcctgcactgcccccaggggcagtcgggg 1020

Qy   2113 ATGGGCCCCCCAGAGTGGATTTCCCTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCG 2172
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Db  1021 atgggccccccagagtggatttccctcgatctcgactccgcttcaaggagaagcttggcg 1080
Qy  2173 AGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTC 2232
Db  1081 agggccagtttggggaggtgcacctgtgtgaggtcgacagccctcaagatctggtcagtc 1140
Qy  2233 TTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTAC 2292
Db  1141 ttgatttccccttaatgtgcgtaagggacacccttgctggtagctgtcaagatcttac 1200
Qy  2293 GGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAG 2352
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Qy  2353 AGGTGAAGATCATGTCGAGGCTCAGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTG 2412
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Qy  2413 TGCAGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCAGT 2472
Db  1303 tgcaggacgacccccctctgcatgattactgactacatggagaacggcgacctcaaccagt 1362
Qy  2473 TCCTCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGG 2532
Db  1363 tcctcagtgcccaccagctggaggacaaggcagccgaggggcccctggggacgggcagg 1422
Qy  2533 CTGCGCAGGGGCCCACCATCAGCTACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCT 2592
Db  1423 ctgcgcaggggcccaccatcagctacccaatgctgctgcatgtggcagcccagatcgcct 1482
Qy  2593 CCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATCGGGACCTGGCCACGCGGAACT 2652
Db  1483 ccggcatgcgctatctggccacactcaactttgtacatcgggacctggccacgcggaact 1542
Qy  2653 GCCTAGTTGGGGAAAATTTCACCATCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCT 2712
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Db  1603 atgctggggactattaccgtgtgcagggccgggcagtgctgcccatccgctggatggcct 1662
Qy  2773 GGGAGTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGA 2832
Db  1663 gggagtgcatcctcatggggaagttcacgactgcgagtgacgtgtgggcctttggtgtga 1722
Qy  2833 CCCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGC 2892
Db  1723 ccctgtgggaggtgctgatgctctgtagggcccagcccttgggcagctcaccgacgagc 1782
Qy  2893 AGGTCATCGAGAACGCGGGGGAGTTCTTCCGGGACCAGGGCCGGCAGGTGTACCTGTCCC 2952
Db  1783 aggtcatcgagaacgcgggggagttcttccgggaccagggccggcaggtgtacctgtccc 1842
Qy  2953 GGCCGCCTGCCTGCCCGCAGGGCCTATATGAGCTGATGCTTCGGTGCTGGAGCCGGGAGT 3012
Db  1843 ggccgcctgcctgcccgca-ggcytatatgagctgatgcttcggtgctggagccgggagt 1901
Qy  3013 CTGAGCAGCGACCACCCTTTTCCCAGCTGCATCGGTTCCTGGCAGAGGATGCACTCAACA 3072
Db  1902 ctgagcagcgaccacccttttcccagctgcatcggttcctggcagaggatgcactcaaca 1961
Qy  3073 CGGTGTGAATCACACATCCAGCTGCCCCTCCCTCAGGGAGTGATCCAGGGGAAGCCAGTG 3132
Db  1962 cggtgtgaatcacacatccagctgcccctccctcagggagcgatccaggggaagccagtg 2021
Qy  3133 ACACTAAAACAAGAGGACACAATGGCACCTCTGCCCTTCCCCTCCCGACAGCCCATCACC 3192
Db  2022 acactaaaacaagaggacacaatggcacctctgcccttccccctcccgacagcccatcacc 2081
Qy  3193 TCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCACCCAGGGAGCTGATGCCCCTT 3252
Db  2082 tctaatagaggcagtgagactgcaggtgggctgggcccacccagggagctgatgcccctt 2141
Qy  3253 CTCCCCTTCCTGGACACACTCTCATGTCCCCTTCCTGTTCTTCCTTCCTAGAAGCCCCTG 3312
Db  2142 ctccccttcctggacacactctcatgtccccttcctgttcttccttcctagaagccccctg 2201
Qy  3313 TCGCCCACCCAGCTGGTCCTGTGGATGGGATCCTCTCCACCCTCCTCTAGCCATCCCTTG 3372
Db  2202 tcgcccacccagctggtcctgtggatgggatcctctccaccctcctctagccatcccttg 2261
Qy  3373 GGGAAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCCATTGGAGCACCTGGGC 3432
Db  2262 gggaagggtggggagaaatataggatagacactggacatggcccattggagcacctgggc 2321
Qy  3433 CCCACTGGACAACACTGATTCCTGGAGAGGTGGCTGCG-CCCCAGCTTCTCTCTCCCTGT 3491
Db  2322 cccactggacaacactgattcctggagaggtggctgcgccccccagcttctctctccctgt 2381
Qy  3492 CACACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGAAGGAGAGGAAA 3551
Db  2382 cacacactggaccccactggctgagaatctgggggtgaggaggacaagaaggagaggaaa 2441
Qy  3552 ATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCA 3611
Db  2442 atgtttccttgtgcctgctcctgtacttgtcctcagcttgggcttcttcctcctccatca 2501
Qy  3612 CCTGAAACACTGGACCTGGGGGTAGCCCCGCCCCAGCCCTCAGTCACCCCCACTTCCCAC 3671
Db  2502 cctgaaacactggacctgggggtagccccgccccagccctcagtcaccccccacttcccac 2561
Qy  3672 TTGCAGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAGTAAATATTGGG 3731
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Qy  3732 ATTGGGGGGAAAGAGGGAGCAACGGCCCATAGCCTTGGGGTTGGACATCTCTAGTGTAGC 3791
Db  2622 attgggggggaaagagggagcaacggcccatagccttggggttggacatctctagtgtagc 2681
Qy  3792 TGCCACATTGATTTTTCTATAATCACTTGGGGTTTGTACATTTTTGGGGGGAGAGACACA 3851
Db  2682 tgccacattgatttttctataatcacttggggtttgtacatttttgggggggagagacaca 2741
Qy  3852 GATTTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAATCCCCTGCACTAGGCAG 3911
Db  2742 gatttttacactaatatatggacctagcttgaggcaattttaatccccctgcactaggcag 2801
Qy  3912 GTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAAAA 3953
Db  2802 gtaataataaaggttgagttttccacaaaaaaaaaaaaaaaa 2843
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RESULT   7
AAH33198
ID   AAH33198 standard; cDNA; 2861 BP.
XX
AC   AAH33198;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:254.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 6; ss.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
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PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG73767.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 2388-2389; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 2861 BP; 567 A; 899 C; 800 G; 589 T; 6 other;

Query Match 70.3%; Score 2783.6; DB 22; Length 2861;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2833; Conservative 5; Mismatches 4; Indels 20; Gaps 3;

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Qy   1093 GGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGA 1152
          ||  ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggcacarccacagcttctccagtggctatgtggagatggagtttgagtttgaccggctga 60

Qy   1153 GGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGGGAGCCCGTCTGC 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gggccttccaggctatgcaggtccactgtaacaacatgcacacgctgggagcccgtctgc 120

Qy   1213 CTGGCGGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCA 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ctggcggggtggaatgtcgcttccggcgtggccctgccatggcctgggagggggagccca 180

Qy   1273 TGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCC 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 tgcgccacaacctagggggcaacctgggggaccccagagcccgggctgtctcagtgcccc 240

Qy   1333 TTGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTAC 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ttggcggccgtgtggctcgctttctgcagtgccgcttcctctttgcggggcccctggttac 300

Qy   1393 TCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAG 1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 tcttcagcgaaatctccttcatctctgatgtggtgaacaattcctctccggcactgggag 360

Qy   1453 GCACCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCAACTTCAGCAGCT 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gcaccttcccgccagccccctggtggccgcctggcccacctcccaccaacttcagcagct 420

Qy   1513 TGGAGCTGGAGCCCAGAGGCCAGCAGCCCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCA 1572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tggagctggagcccagaggccagcagcccgtggccaaggccgaggggagcccgaccgcca 480

Qy   1573 TCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCATCATTGCCCTCATGC 1632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 tcctcatcggctgcctggtggccatcatcctgctcctgctgctcatcattgccctcatgc 540

Qy   1633 TCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGG 1692
          ||||||||||||||||||||||||:|||||||||||:||||||||||||||||||||||||
Db    541 tctggcggctgcactggcgcaggytcctcagcaaggytgaacggagggtgttggaagagg 600

Qy   1693 AGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCAACAACCGCCCAGGTC 1752
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Qy   1753 CTAGAGAGCCACCCCCGTACCAGGAGCCCCGGCCTCGTGGGAATCCGCCCCCACTCCGCTC 1812
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Db    661 ctagagagccacccccgtaccaggagccccggcctcgtgggaatccgccccactcygctc 720

Qy   1813 CCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCTACCGCCTCCTTCTGG 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 cctgtgtccccaatggctctgcgttgctgctctccaatccagcctaccgcctccttctgg 780

Qy   1873 CCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCCCACACCCGCCTGGGCCAAACCCA 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ccacttacgcccgtcccctcgaggcccgggcccccccacacccgcctgggccaaaccca 840

Qy   1933 CCAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTC 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ccaacacccaggcctacagtggggactatatggagcctgagaagccaggcgccccgcttc 900

Qy   1993 TGCCCCCACCTCCCCAGAACAGCGTCCCCCATTATGCCGAGGCTGACATTGTTACCCTGC 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 tgcccccacctccccagaacagcgtccccccattatgccgaggctgacattgttaccctgc 960

Qy   2053 AGGGCGTCACCGGGGGCAACACCTATGCTGTGCCTGCACTGCCCCCAGGGGCAGTCGGGG 2112
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Db    961 agggcgtcaccgggggcaacacctatgctgtgcctgcactgcccccaggggcagtcgggg 1020

Qy   2113 ATGGGCCCCCCAGAGTGGATTTCCCTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCG 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 atgggcccccagagtggatttccctcgatctcgactccgcttcaaggagaagcttggcg 1080

Qy   2173 AGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTC 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 agggccagtttggggaggtgcacctgtgtgaggtcgacagccctcaagatctggtcagtc 1140

Qy   2233 TTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTAC 2292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ttgatttccccttaatgtgcgtaagggacacccttgctggtagctgtcaagatcttac 1200

Qy   2293 GGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAG 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ggccagatgccaccaagaatg----------ccaggaatgatttcctgaaag 1242

Qy   2353 AGGTGAAGATCATGTCGAGGCTCAAGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTG 2412
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Qy   2413 TGCAGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCAGT 2472
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Qy   2473 TCCTCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGG 2532
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Db    1363 tcctcagtgcccaccagctggaggacaaggcagccgagggggcccctggggacgggcagg 1422

Qy   2533 CTGCGCAGGGGCCCACCATCAGCTACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCT 2592
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Qy   2593 CCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATCGGGACCTGGCCACGCGGAACT 2652
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Db    1483 ccggcatgcgctatctggccacactcaactttgtacatcgggacctggccacgcggaact 1542

Qy   2653 GCCTAGTTGGGGAAAATTTCACCATCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCT 2712
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Qy   2773 GGGAGTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGA 2832
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Qy   2833 CCCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGC 2892
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Qy   3133 ACACTAAAACAAGAGGACACAATGGCACCTCTGCCCTTCCCCTCCCGACAGCCCATCACC 3192
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Qy   3193 TCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCACCCAGGGAGCTGATGCCCCTT 3252
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Qy   3433 CCCACTGGACAACACTGATTCCTGGAGAGGTGGCTGCG-CCCCAGCTTCTCTCTCCCTGT 3491
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Qy   3492 CACACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGAAGGAGAGGAAA 3551
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Qy   3552 ATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCA 3611
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Qy   3672 TTGCAGTCTTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAGTAAATATTGGG 3731
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Qy   3732 ATTGGGGGGAAAGAGGGAGCAACGGCCCATAGCCTTGGGGTTGGACATCTCTAGTGTAGC 3791
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Db   2622 attgggggggaaagagggagcaacggcccatagccttggggttggacatctctagtgtagc 2681

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Qy   3852 GATTTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAATCCCCTGCACTAGGCAG 3911
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Qy   3912 GTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAAAA 3953
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Db   2802 gtaataataaaggttgagttttccacaaaaaaaaaaaaaaaa 2843
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RESULT 8
AAV48292
ID AAV48292 standard; cDNA; 3096 BP.
XX
AC AAV48292;
XX
DT 16-NOV-1998 (first entry)
XX
DE Discoidin domain receptor 2 gene.
XX
KW Discoidin domain receptor; transformation; metastasis; collagen; ss;
KW Cleidocranial displasia; Sickler syndrome; extracellular matrix; MMP-1.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	354..2921
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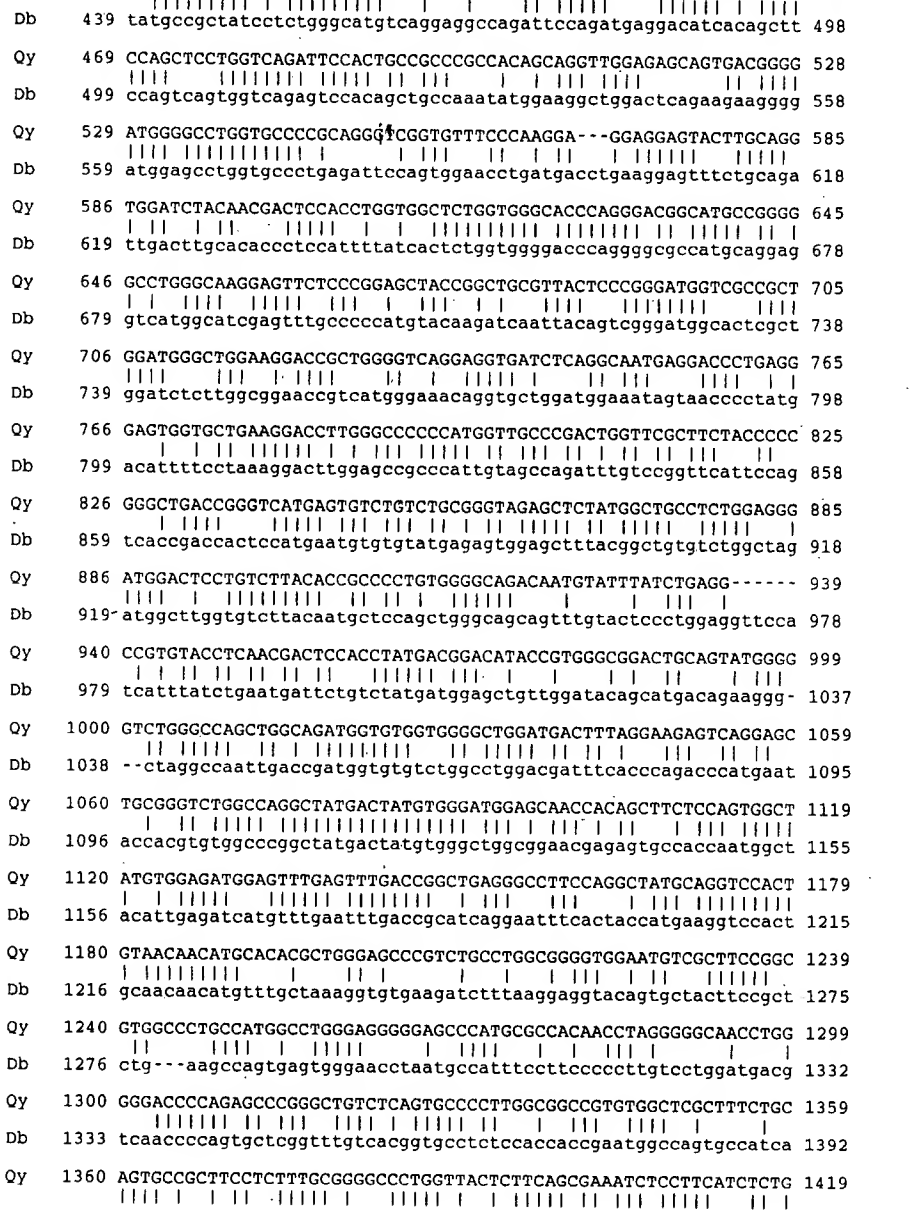
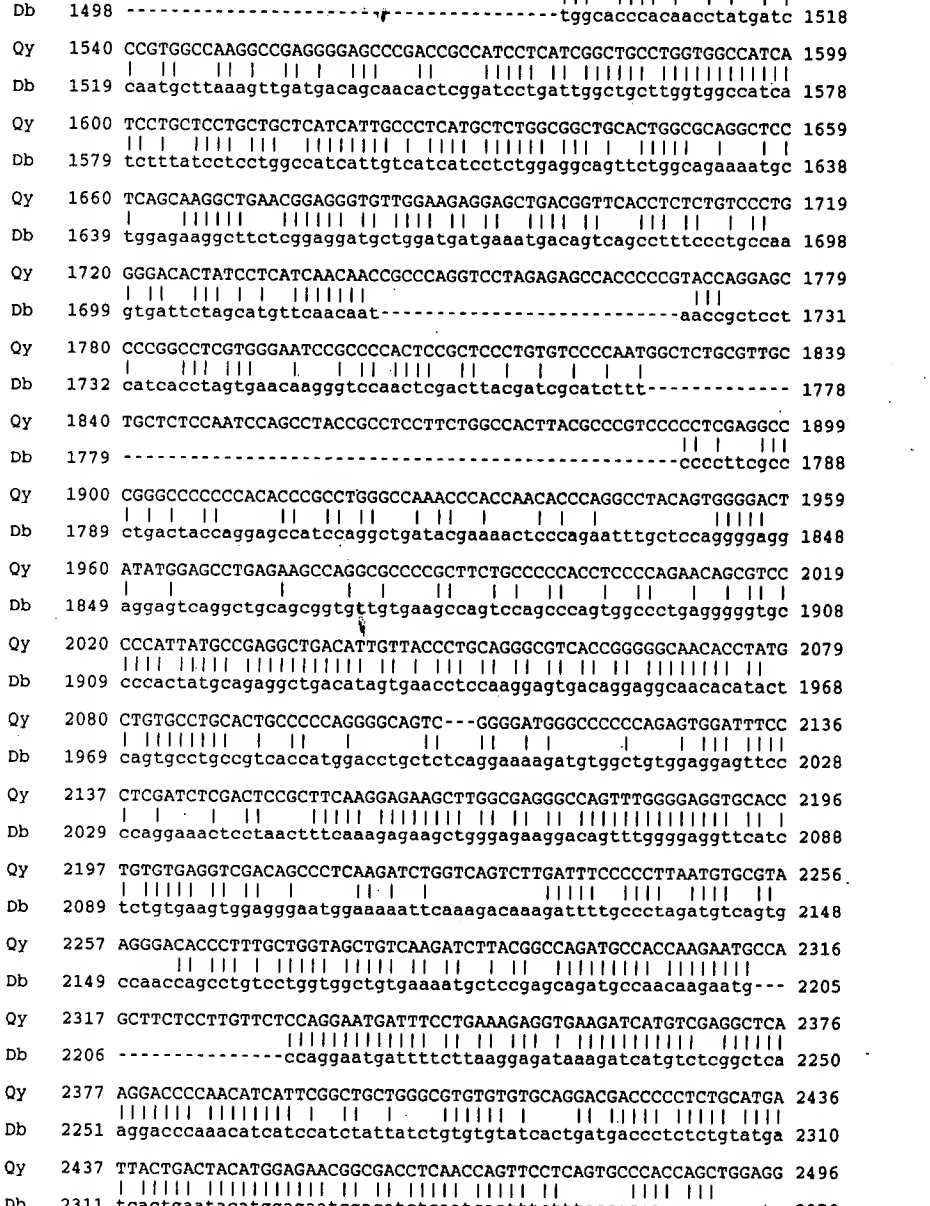
FT		/product= "Discoidin domain receptor"
FT	sig_peptide	354..416
FT		/*tag= b
FT	mat_peptide	417..2918
FT		/*tag= c

XX
PN WO9834954-A2.
XX
PD 13-AUG-1998.
XX
PF 05-FEB-1998; 98WO-CA00093.
XX
PR 06-FEB-1997; 97US-0041578.
XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Pawson A, Vogel W;
XX
DR WPI; 1998-447168/38.
DR P-PSDB; AAW77114.
XX
PT Novel ligands of discoidin domain receptor tyrosine kinase,
PT especially collagen - useful for treating e.g. metastasis,
PT cleidocranial displasia or Sickler syndrome
XX
PS Disclosure; Fig 22a; 115pp; English.
XX
CC The DDR can be used to identify and evaluate substances which affect DDR
CC receptor tyrosine kinase signalling pathways in the cell. Compounds
CC which modulate such signalling pathways can be used to alter
CC transformation or metastasis in mammals, to treat conditions involving
CC structural or functional deregulation of collagens, e.g. Cleidocranial
CC displasia or Sickler syndrome, conditions requiring modulation of
CC extracellular matrix synthesis, degradation or remodelling, or to treat
CC conditions needing modulation of MMP-1 expression such as wound healing.
XX
SQ Sequence 3096 BP; 762 A; 791 C; 752 G; 791 T; 0 other;

Query Match 16.2%; Score 642; DB 19; Length 3096;

Best Local Similarity 56.5%; Pred. No. 1.1e-130;
Matches 1534; Conservative 0; Mismatches 975; Indels 207; Gaps 10;





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Qy   2497 ACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCT 2556
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Db   2371 attcttcctccagcg--------------------------atgtacgcactgtcagtt 2403

Qy   2557 ACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCTCCGGCATGCGCTATCTGGCCACAC 2616
          || | |  |||  |  | ||||  |||| || ||||| ||||||   || ||  || | |
Db   2404 acaccaatctgaagtttatggctacccaaattgcctctggcatgaagtacctttcctctc 2463

Qy   2617 TCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCA 2676
          | || ||||| || || || |||||||| || |||||  |||| ||  | || | ||| |
Db   2464 ttaattttgttcaccgagatctggccacacgaaactgtttagtgggtaagaactacacaa 2523

Qy   2677 TCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTGC 2736
          |||| || || |||||||| |||||| ||||||| ||   ||| ||||||||||| | |
Db   2524 tcaagatagctgactttggaatgagcaggaacctgtacagtggtgactattaccggatcc 2583

Qy   2737 AGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGT 2796
          |||||||||||||||| || |||||||||||| | |||||| | ||| |  |||| ||||
Db   2584 agggccgggcagtgctccctatccgctggatgtcttgggagagtatcttgctgggcaagt 2643

Qy   2797 TCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCT 2856
          |||| || || ||||| |||||||||||||| || ||  ||||||||    | |   | |
Db   2644 tcactacagcaagtgatgtgtgggcctttggggttactttgtgggagactttcacctttt 2703

Qy   2857 GTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGT 2916
          ||   |  |||||||  |   |||||  | || || ||||| || |||||  | || ||||
Db   2704 gtcaagaacagccctattcccagctgtcagatgaacaggttattgagaatactggagagt 2763

Qy   2917 TCTTCCGGGACCAGGGCCGGCAGGTGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCC 2976
          |||||||  ||||| ||  |||||  |||||  | |  ||  |    || ||  |
Db   2764 tcttccgagaccaagggaggcagacttacctccctcaaccagccatttgtcctgactctg 2823

Qy   2977 TATATGAGCTGATGCTTCGGTGCTGGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCC 3036
          | ||| ||||||||||  | ||||||||  | ||  |  || | || ||  | ||
Db   2824 tgtataagctgatgctcagctgctggagaagagatacgaagaaccgtccctcattccaag 2883

Qy   3037 AGCTGCATCGGTTCCT 3052
          |  | || |   | ||
Db   2884 aaatccaccttctgct 2899


RESULT   9
AAQ92521
ID   AAQ92521 standard; cDNA to mRNA; 3157 BP.
XX
AC   AAQ92521;
XX
DT   26-NOV-1995  (first entry)
XX
DE   Human colonic adenocarcinoma kinase 2 (CCK-2) cDNA.
XX
KW   Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;
KW   receptor tyrosine kinase; colonic adenocarcinoma kinase 2; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             370..2937
FT                   /*tag= a
XX
PN   WO9514088-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03797.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224054/29.
DR   P-PSDB; AAR75503.
XX
PT   New nucleic acid encoding MCK-10 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies useful
PT   for diagnosis and treatment of proliferative disease, esp. cancer,
PT   and for screening modulators
XX
PS   Disclosure; Page 56-57; 115pp; English.
XX
CC   A member of the mammary carcinomal kinase 10 (MCK-10) receptor
CC   tyrosine kinase family was identified using a PCR (with two degenerate
CC   oligo primer pools based on conserved sequences of the kinase domain of
CC   receptor tyrosine kinases) and cDNA prepd. from colonic
CC   adenocarcinoma RNA. The nt sequence of the novel receptor,
CC   designated CCK-2, is given in AAQ92521 and the deduced AA sequence in
CC   AAR75503. Analysis of the CCK-2 nt and AA sequence indicated
CC   significant homology with MCK-10 throughout the extracellular,
CC   transmembrane and intracellular regions. The regions of homology
CC   extend into the N-terminus consensus sequence for the discoidin I
CC   like family of proteins.
XX
SQ   Sequence 3157 BP; 790 A; 802 C; 759 G; 806 T; 0 other;


  Query Match             16.2%;  Score 642;  DB 16;  Length 3157;
  Best Local Similarity   56.5%;  Pred. No. 1.1e-130;
  Matches 1534;  Conservative    0;  Mismatches  975;  Indels  207;  Gaps   10;

Qy    349 TGCTGCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCA 408
          || ||||| || || ||     |        |      || |  ||  || |||| || |
Db    395 tggtgctgttcctgctgctgcctatcttgagttctgcaaaagctcaggttaatccagcta 454

Qy    409 AGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTT 468
          |||||||||  | |||||||||    |   |    || |||||    |||||| | ||||
Db    455 tatgccgctatcctctgggcatgtcaggaggccagattccagatgaggacatcacagctt 514

Qy    469 CCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGG 528
          ||||    |||||||| ||||| || |||   |  | ||| ||||       || ||||
Db    515 ccagtcagtggtcagagtccacagctgccaaatatggaaggctggactcagaagaagggg 574

Qy    529 ATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGA---GGAGGAGTACTTGCAGG 585
          |||| |||||||||| |      | |||   ||  | ||  | ||||||   |||||
Db    575 atggagcctggtgccctgagattccagtggaacctgatgacctgaaggagtttctgcaga 634

Qy    586 TGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGG 645
          | ||  | ||    |||||  |  | ||||||||||| |||||||| || ||||| || |
Db    635 ttgacttgcacaccctccattttatcactctggtggggacccaggggcgccatgcaggag 694

Qy    646 GCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCT 705
          | |  |||| ||||| |||  | |||  | |   ||||   ||||||||    ||||
Db    695 gtcatggcatcgagtttgcccccatgtacaagatcaattacagtcgggatggcactcgct 754

Qy    706 GGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGG 765
          ||||    |||  | ||||    ||  |  ||||| |    || |||    |||| | |
Db    755 ggatctcttggcggaaccgtcatgggaaacaggtgctggatggaaatagtaacccctatg 814

Qy    766 GAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCCC 825
            | | || |||||| | | ||| ||||| || ||| || | || || ||| ||
Db    815 acattttcctaaaggacttggagccgcccattgtagccagatttgtccggttcattccag 874

Qy    826 GGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGG 885
            | ||||    ||||| ||| ||| || | || ||||| || |||||  |||||   |
Db    875 tcaccgaccactccatgaatgtgtgtatgagagtggagctttacggctgtgtctggctag 934

Qy    886 ATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGG------ 939
          ||||  |  |||||||||  || || |  ||||||    |     |  |||  |
Db    935 atggcttggtgtcttacaatgctccagctgggcagcagtttgtactccctggaggttcca 994

Qy    940 CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGG 999
            | | || || || || ||   |||||| ||| |  |    | | ||   | |||
Db    995 tcatttatctgaatgattctgtctatgatggagctgttggatacagcatgacagaaggg- 1053
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Qy   1000 GTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGC 1059
Db   1054 --ctaggccaattgaccgatggtgtgtctggcctggacgatttcacccagacccatgaat 1111

Qy   1060 TGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCT 1119
Db   1112 accacgtgtggcccggctatgactatgtgggctggcggaacgagagtgccaccaatggct 1171

Qy   1120 ATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACT 1179
Db   1172 acattgagatcatgtttgaatttgaccgcatcaggaatttcactaccatgaaggtccact 1231

Qy   1180 GTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGC 1239
Db   1232 gcaacaacatgtttgctaaaggtgtgaagatctttaaggaggtacagtgctacttccgct 1291

Qy   1240 GTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGG 1299
Db   1292 ctg---aagccagtgagtgggaacctaatgccatttccttcccccttgtcctggatgacg 1348

Qy   1300 GGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGC 1359
Db   1349 tcaaccccagtgctcggtttgtcacggtgcctctccaccaccgaatggccagtgccatca 1408

Qy   1360 AGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTG 1419
Db   1409 agtgtcaataccattttgcagatacctggatgatgttcagtgagatcaccttccaatcag 1468

Qy   1420 ATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGC 1479
Db   1469 atgctgcaatgtacaacaactctgaagccctgcccacctctccta---------------- 1513

Qy   1480 CGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGC 1539
Db   1514 ----------------------------------------tggcacccacaacctatgatc 1534

Qy   1540 CCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCA 1599
Db   1535 caatgcttaaagttgatgacagcaacactcggatcctgattggctgcttggtggccatca 1594

Qy   1600 TCCTGCTCCTGCTGCTCATCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCC 1659
Db   1595 tctttatcctcctggccatcattgtcatcatcctctggaggcagttctggcagaaaatgc 1654

Qy   1660 TCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTG 1719
Db   1655 tggagaaggcttctcggaggatgctggatgatgaaatgacagtcagcctttccctgccaa 1714

Qy   1720 GGGACACTATCCTCATCAACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGC 1779
Db   1715 gtgattctagcatgttcaacaat----------------------------aaccgctcct 1747

Qy   1780 CCCGGCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGC 1839
Db   1748 catcacctagtgaacaagggtccaactcgacttacgatcgcatcttt------------- 1794

Qy   1840 TGCTCTCCAATCCAGCCTACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCC 1899
Db   1795 ----------------------------------------------------ccccttcgcc 1804

Qy   1900 CGGGCCCCCCCACACCCGCCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACT 1959
Db   1805 ctgactaccaggagccatccaggctgatacgaaaactcccagaatttgctccaggggagg 1864

Qy   1960 ATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCC 2019
Db   1865 aggagtcaggctgcagcggtgttgtgaagccagtccagcccagtggccctgaggggggtgc 1924

Qy   2020 CCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATG 2079
Db   1925 cccactatgcagaggctgacatagtgaacctccaaggagtgacaggaggcaacacatact 1984

Qy   2080 CTGTGCCTGCACTGCCCCCAGGGGCAGTC---GGGGATGGGCCCCCCAGAGTGGATTTCC 2136
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Db   1985 cagtgcctgccgtcaccatggacctgctctcaggaaaagatgtggctgtggaggagttcc 2044

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Db   2045 ccaggaaactcctaactttcaaagagaagctgggagaaggacagtttggggaggttcatc 2104

Qy   2197 TGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTA 2256
Db   2105 tctgtgaagtggagggaatggaaaaattcaaagacaaagattttgccctagatgtcagtg 2164

Qy   2257 AGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTACGGCCAGATGCCACCAAGAATGCCA 2316
Db   2165 ccaaccagcctgtcctggtggctgtgaaaatgctccgagcagatgccaacaagaatg--- 2221

Qy   2317 GCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCA 2376
Db   2222 --------------ccaggaatgattttcttaaggagataaagatcatgtctcggctca 2266

Qy   2377 AGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATGA 2436
Db   2267 aggacccaaacatcatccatctattatctgtgtgtatcactgatgaccctctctgtatga 2326

Qy   2437 TTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGG 2496
Db   2327 tcactgaatacatggagaatggagatctcaatcagtttctttcccgccacgagcccccta 2386

Qy   2497 ACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCT 2556
Db   2387 attcttcctccagcg--------------------------atgtacgcactgtcagtt 2419

Qy   2557 ACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCTCCGGCATGCGCTATCTGGCCACAC 2616
Db   2420 acaccaatctgaagtttatggctacccaaattgcctctggcatgaagtacctttcctctc 2479

Qy   2617 TCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCA 2676
Db   2480 ttaattttgttcaccgagatctggccacacgaaactgtttagtgggtaagaactacacaa 2539

Qy   2677 TCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTGC 2736
Db   2540 tcaagatagctgactttggaatgagcaggaacctgtacagtggtgactattaccggatcc 2599

Qy   2737 AGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGT 2796
Db   2600 agggccgggcagtgctccctatccgctggatgtcttgggagagtatcttgctgggcaagt 2659

Qy   2797 TCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCT 2856
Db   2660 tcactacagcaagtgatgtgtgggcctttggggttactttgtgggagactttcacctttt 2719

Qy   2857 GTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGT 2916
Db   2720 gtcaagaacagccctattcccagctgtcagatgaacaggttattgagaatactggagagt 2779

Qy   2917 TCTTCCGGGACCAGGGCCGGCAGGTGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCC 2976
Db   2780 tcttccgagaccaagggaggcagacttacctccctcaaccagccatttgtcctgactctg 2839

Qy   2977 TATATGAGCTGATGCTTCGGTGCTGGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCC 3036
Db   2840 tgtataagctgatgctcagctgctggagaagagatacgaagaaccgtccctcattccaag 2899

Qy   3037 AGCTGCATCGGTTCCT 3052
Db   2900 aaatccaccttctgct 2915
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RESULT 10
AAQ92523
ID AAQ92523 standard; cDNA to mRNA; 3157 BP.
XX
AC AAQ92523;

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XX
DT   26-NOV-1995  (first entry)
XX
DE   Human colonic adenocarcinoma kinase 2 (CCK-2) cDNA.
XX
KW   Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;
KW   receptor tyrosine kinase; colonic adenocarcinoma kinase 2; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             370..2937
FT                   /*tag= a
XX
PN   WO9514089-A.
XX
PD   26-MAY-1995.
XX
PF   16-NOV-1994;   94WO-EP03799.
XX
PR   16-NOV-1993;   93US-0153397.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Alves FHE,  Ullrich A;
XX
DR   WPI; 1995-224055/29.
DR   P-PSDB; AAR75505.
XX
PT   New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
PT   derived vectors, transformed cells, proteins and antibodies, useful
PT   for diagnosis and treatment of proliferative and nervous system
PT   diseases and for screening modulators
XX
PS   Disclosure; Page 73-74; 115pp; English.
XX
CC   A member of the mammary carcinomal kinase 10 (MCK-10) receptor
CC   tyrosine kinase family was identified using a PCR (with two
CC   degenerate oligo primer pools based on conserved sequences of the
CC   kinase domains of receptor tyrosine kinases) and cDNA prepd. from
CC   colonic adenocarcinoma RNA. The nt sequence of the novel receptor,
CC   designated CCK-2, is given in AAQ92523 and the deduced AA sequence in
CC   AAR75505. Analysis of CCK-2 nt and AA sequences indicated significant
CC   homology with MCK-10 throughout the extracellular, transmembrane
CC   and intracellular regions. The regions of homology extend into the
CC   N-terminus consensus seuence fothe discoidin I like family of
CC   proteins. CCK-2 was predominantly found in all stromal cells
CC   whereas MCK-10 expression was stronglyu confined to neoplastic
CC   cells themselves. Between the two RTKs, the juxtamembrane region
CC   is the region of most extensive sequence divergence.
XX
SQ   Sequence 3157 BP; 790 A; 802 C; 759 G; 806 T; 0 other;

  Query Match            16.2%;  Score 642;  DB 16;  Length 3157;
  Best Local Similarity  56.5%;  Pred. No. 1.1e-130;
  Matches 1534;  Conservative    0;  Mismatches  975;  Indels  207;  Gaps   10;

Qy    349 TGCTGCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCA 408
Db    395 tggtgctgttcctgctgctgcctatcttgagttctgcaaaagctcaggttaatccagcta 454

Qy    409 AGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTT 468
Db    455 tatgccgctatcctctgggcatgtcaggaggccagattccagatgaggacatcacagctt 514

Qy    469 CCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGG 528
Db    515 ccagtcagtggtcagagtccacagctgccaaatatggaaggctggactcagaagaagggg 574

Qy    529 ATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGA---GGAGGAGTACTTGCAGG 585
Db    575 atggagcctggtgccctgagattccagtggaacctgatgacctgaaggagtttctgcaga 634

Qy    586 TGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGG 645
Db    635 ttgacttgcacaccctccattttatcactctggtggggacccaggggcgccatgcaggag 694

Qy    646 GCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCT 705
Db    695 gtcatggcatcgagtttgcccccatgtacaagatcaattacagtcgggatggcactcgct 754

Qy    706 GGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGG 765
Db    755 ggatctcttggcggaaccgtcatgggaaacaggtgctggatggaaatagtaacccctatg 814

Qy    766 GAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCCC 825
Db    815 acattttcctaaaggacttggagccgcccattgtagccagatttgtccggttcattccag 874

Qy    826 GGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGG 885
Db    875 tcaccgaccactccatgaatgtgtgtatgagagtggagctttacggctgtgtctggctag 934

Qy    886 ATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGG------ 939
Db    935 atggcttggtgtcttacaatgctccagctgggcagcagtttgtactccctggaggttcca 994

Qy    940 CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGG 999
Db    995 tcatttatctgaatgattctgtctatgatggagctgttggatacagcatgacagaaggg- 1053

Qy   1000 GTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGC 1059
Db   1054 --ctaggccaattgaccgatggtgtgtctggcctggacgatttcacccagacccatgaat 1111

Qy   1060 TGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCT 1119
Db   1112 accacgtgtggcccggctatgactatgtgggctggcggaacgagagtgccaccaatggct 1171

Qy   1120 ATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACT 1179
Db   1172 acattgagatcatgtttgaatttgaccgcatcaggaatttcactaccatgaaggtccact 1231

Qy   1180 GTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGC 1239
Db   1232 gcaacaacatgtttgctaaaggtgtgaagatctttaaggaggtacagtgctacttccgct 1291

Qy   1240 GTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGG 1299
Db   1292 ctg---aagccagtgagtgggaacctaatgccatttccttccccccttgtcctggatgacg 1348

Qy   1300 GGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGC 1359
Db   1349 tcaaccccagtgctcggtttgtcacggtgcctctccaccaccgaatggccagtgccatca 1408

Qy   1360 AGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTG 1419
Db   1409 agtgtcaataccattttgcagatacctggatgatgttcagtgagatcaccttccaatcag 1468

Qy   1420 ATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGC 1479
Db   1469 atgctgcaatgtacaacaactctgaagccctgcccacctctcta---------------- 1513

Qy   1480 CGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGC 1539
Db   1514 ----------------------------------------tggcacccacaacctatgatc 1534

Qy   1540 CCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCA 1599
Db   1535 caatgcttaaagttgatgacagcaacactcggatcctgattggctgcttggtggccatca 1594

Qy   1600 TCCTGCTCCTGCTGCTCATCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCC 1659
Db   1595 tctttatcctcctggccatcattgtcatcatcctctggaggcagttctggcagaaaatgc 1654
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Qy   1660 TCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTG 1719
Db   1655 tggagaaggcttctcggaggatgctggatgatgaaatgacagtcagcctttccctgccaa 1714

Qy   1720 GGGACACTATCCTCATCAACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGC 1779
Db   1715 gtgattctagcatgttcaacaat--------------------------aaccgctcct 1747

Qy   1780 CCCGGCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGC 1839
Db   1748 catcacctagtgaacaagggtccaactcgacttacgatcgcatcttt------------ 1794

Qy   1840 TGCTCTCCAATCCAGCCTACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCC 1899
Db   1795 ----------------------------------------------------ccccttcgcc 1804

Qy   1900 CGGGCCCCCCCACACCCGCCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACT 1959
Db   1805 ctgactaccaggagccatccaggctgatacgaaaactcccagaatttgctccaggggagg 1864

Qy   1960 ATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCC 2019
Db   1865 aggagtcaggctgcagcggtgttgtgaagccagtccagcccagtggccctgaggggtgc 1924

Qy   2020 CCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATG 2079
Db   1925 cccactatgcagaggctgacatagtgaacctccaaggagtgacaggaggcaacacatact 1984

Qy   2080 CTGTGCCTGCACTGCCCCCAGGGGCAGTC---GGGGATGGGCCCCCCAGAGTGGATTTCC 2136
Db   1985 cagtgcctgccgtcaccatggacctgctctcaggaaaagatgtggctgtggaggagttcc 2044

Qy   2137 CTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACC 2196
Db   2045 ccaggaaactcctaactttcaaagagaagctgggagaaggacagtttggggaggttcatc 2104

Qy   2197 TGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTA 2256
Db   2105 tctgtgaagtggagggaatggaaaaattcaaagacaaagattttgccctagatgtcagtg 2164

Qy   2257 AGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTACGGCCAGATGCCACCAAGAATGCCA 2316
Db   2165 ccaaccagcctgtcctggtggctgtgaaaatgctccgagcagatgccaacaagaatg--- 2221

Qy   2317 GCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCA 2376
Db   2222 --------------ccaggaatgattttcttaaggagataaagatcatgtctcggctca 2266

Qy   2377 AGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATGA 2436
Db   2267 aggacccaaacatcatccatctattatctgtgtgtatcactgatgaccctctctgtatga 2326

Qy   2437 TTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGG 2496
Db   2327 tcactgaatacatggagaatggagatctcaatcagtttctttcccgccacgagcccccta 2386

Qy   2497 ACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCT 2556
Db   2387 attcttcctccagcg------------------------atgtacgcactgtcagtt 2419

Qy   2557 ACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCTCCGGCATGCGCTATCTGGCCACAC 2616
Db   2420 acaccaatctgaagtttatggctacccaaattgcctctggcatgaagtacctttcctctc 2479

Qy   2617 TCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCA 2676
Db   2480 ttaattttgttcaccgagatctggccacacgaaactgtttagtgggtaagaactacacaa 2539

Qy   2677 TCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTGC 2736
Db   2540 tcaagatagctgactttggaatgagcaggaacctgtacagtggtgactattaccggatcc 2599

Qy   2737 AGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGT 2796
Db   2600 agggccgggcagtgctccctatccgctggatgtcttgggagagtatcttgctgggcaagt 2659

Qy   2797 TCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCT 2856
Db   2660 tcactacagcaagtgatgtgtgggcctttggggttactttgtgggagactttcacctttt 2719

Qy   2857 GTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGT 2916
Db   2720 gtcaagaacagccctattcccagctgtcagatgaacaggttattgagaatactggagagt 2779

Qy   2917 TCTTCCGGGACCAGGGCCGGCAGGTGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCC 2976
Db   2780 tcttccgagaccaagggaggcagacttacctccctcaaccagccatttgtcctgactctg 2839

Qy   2977 TATATGAGCTGATGCTTCGGTGCTGGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCC 3036
Db   2840 tgtataagctgatgctcagctgctggagaagagatacgaagaaccgtccctcattccaag 2899

Qy   3037 AGCTGCATCGGTTCCT 3052
Db   2900 aaatccaccttctgct 2915
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RESULT 11
AAT93784
ID AAT93784 standard; cDNA; 3157 BP.
XX
AC AAT93784;
XX
DT 16-FEB-1998 (first entry)
XX
DE CCK-2, a human mammary carcinoma kinase 10 MCK-10) family member, cDNA.
XX
KW Mammary carcinoma kinase; MCK-10; CCK-2; receptor tyrosine kinase;
KW proliferative disease; cancer; MCK-10 activity; aberrant expression; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 370..2934
FT /*tag= a
XX
PN US5677144-A.
XX
PD 14-OCT-1997.
XX
PF 08-NOV-1994; 94US-0336343.
XX
PR 16-NOV-1993; 93US-0153397.
XX
PA (ALVE/) ALVES F H E.
PA (ULLR/) ULLRICH A.
XX
PI Alves FHE, Ullrich A;
XX
DR WPI; 1997-511869/47.
DR P-PSDB; AAW34671.
XX
PT Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
PT for it, useful for cancer diagnosis
XX
PS Claim 9; Fig 3; 70pp; English.
XX
CC The present sequence represents the cDNA sequence of human CCK-2, a
CC member of the mammary carcinoma kinase 10 (MCK-10, AAT93785) family of
CC receptor tyrosine kinases. Expression of CCK-2 is associated with
CC proliferative diseases such as cancer. The CCK-2 gene was identified by
CC PCR and a cDNA prepared from colonic adenocarcinoma RNA. CCK-2 is
CC expressed in a wide variety of cancer cell lines and tumour tissue. The
CC CCK-2 nucleic acids can be used for diagnostic purposes to detect
CC aberrant expression of CCK-2 genes. Engineered cell lines, containing
CC recombinant vectors with the present sequence, are useful for producing

```
CC   infectious retroviral particles. The cell lines may also be used to
CC   evaluate and screen drugs involved in CCK-2 activation and regulation.
XX
SQ   Sequence 3157 BP; 790 A; 802 C; 759 G; 806 T; 0 other;

  Query Match             16.2%;  Score 642;  DB 18;  Length 3157;
  Best Local Similarity   56.5%;  Pred. No. 1.1e-130;
  Matches 1534;  Conservative    0;  Mismatches  975;  Indels  207;  Gaps   10;

Qy     349 TGCTGCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCA 408
Db     395 tggtgctgttcctgctgctgcctatcttgagttctgcaaaagctcaggttaatccagcta 454

Qy     409 AGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTT 468
Db     455 tatgccgctatcctctgggcatgtcaggaggccagattccagatgaggacatcacagctt 514

Qy     469 CCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGG 528
Db     515 ccagtcagtggtcagagtccacagctgccaaatatggaaggctggactcagaagaagggg 574

Qy     529 ATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGA---GGAGGAGTACTTGCAGG 585
Db     575 atggagcctggtgccctgagattccagtggaacctgatgacctgaaggagtttctgcaga 634

Qy     586 TGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGG 645
Db     635 ttgacttgcacaccctccattttatcactctggtggggacccaggggcgccatgcaggag 694

Qy     646 GCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCT 705
Db     695 gtcatggcatcgagtttgcccccatgtacaagatcaattacagtcgggatggcactcgct 754

Qy     706 GGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGG 765
Db     755 ggatctcttggcggaaccgtcatgggaaacaggtgctggatggaaatagtaacccctatg 814

Qy     766 GAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCCC 825
Db     815 acattttcctaaaggacttggagccgcccattgtagccagatttgtccggttcattccag 874

Qy     826 GGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGG 885
Db     875 tcaccgaccactccatgaatgtgtgtatgagagtggagctttacggctgtgtctggctag 934

Qy     886 ATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGG------ 939
Db     935 atggcttggtgtcttacaatgctccagctgggcagcagtttgtactccctggaggttcca 994

Qy     940 CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGG 999
Db     995 tcatttatctgaatgattctgtctatgatggagctgttggatacagcatgacagaaggg- 1053

Qy    1000 GTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGC 1059
Db    1054 --ctaggccaattgaccgatggtgtgtctggcctggacgatttcacccagacccatgaat 1111

Qy    1060 TGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCT 1119
Db    1112 accacgtgtggcccggctatgactatgtgggctggcggaacgagagtgccaccaatggct 1171

Qy    1120 ATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACT 1179
Db    1172 acattgagatcatgtttgaatttgaccgcatcaggaatttcactaccatgaaggtccact 1231

Qy    1180 GTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGC 1239
Db    1232 gcaacaacatgtttgctaaaggtgtgaagatctttaaggaggtacagtgctacttccgct 1291

Qy    1240 GTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGG 1299
Db    1292 ctg---aagccagtgagtgggaacctaatgccatttccttccccccttgtcctggatgacg 1348

Qy    1300 GGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGC 1359
Db    1349 tcaaccccagtgctcggtttgtcacggtgcctctccaccaccgaatggccagtgccatca 1408

Qy    1360 AGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTG 1419
Db    1409 agtgtcaataccatttttgcagatacctggatgatgttcagtgagatcaccttccaatcag 1468

Qy    1420 ATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGC 1479
Db    1469 atgctgcaatgtacaacaactctgaagccctgcccacctctcctaa-------------- 1513

Qy    1480 CGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGC 1539
Db    1514 ----------------------------------------tggcacccacaacctatgatc 1534

Qy    1540 CCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCA 1599
Db    1535 caatgcttaaagttgatgacagcaacactcggatcctgattggctgcttggtggccatca 1594

Qy    1600 TCCTGCTCCTGCTGCTCATCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCC 1659
Db    1595 tctttatcctcctggccatcattgtcatcatcctctggaggcagttctggcagaaaatgc 1654

Qy    1660 TCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTG 1719
Db    1655 tggagaaggcttctcggaggatgctggatgatgaaatgacagtcagcctttcctgccaa 1714

Qy    1720 GGGACACTATCCTCATCAACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGC 1779
Db    1715 gtgattctagcatgttcaacaat----------------------------aaccgctcct 1747

Qy    1780 CCCGGCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGC 1839
Db    1748 catcacctagtgaacaagggtccaactcgacttacgatcgcatcttt------------ 1794

Qy    1840 TGCTCTCCAATCCAGCCTACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCC 1899
Db    1795 ----------------------------------------------------ccccttcgcc 1804

Qy    1900 CGGGCCCCCCCACACCCGCCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACT 1959
Db    1805 ctgactaccaggagccatccaggctgatacgaaaactcccagaatttgctccaggggagg 1864

Qy    1960 ATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCC 2019
Db    1865 aggagtcaggctgcagcggtgttgtgaagccagtccagcccagtggccctgaggggtgc 1924

Qy    2020 CCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATG 2079
Db    1925 cccactatgcagaggctgacatagtgaacctccaaggagtgacaggaggcaacacatact 1984

Qy    2080 CTGTGCCTGCACTGCCCCCAGGGGCAGTC---GGGGATGGGCCCCCCAGAGTGGATTTCC 2136
Db    1985 cagtgcctgccgtcaccatggacctgctctcaggaaaagatgtggctgtggaggagttcc 2044

Qy    2137 CTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACC 2196
Db    2045 ccaggaaactcctaactttcaaagagaagctgggagaaggacagtttggggaggttcatc 2104

Qy    2197 TGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTA 2256
Db    2105 tctgtgaagtggagggaatggaaaaattcaaagacaaagattttgccctagatgtcagtg 2164

Qy    2257 AGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTACGGCCAGATGCCACCAAGAATGCCA 2316
Db    2165 ccaaccagcctgtcctggtggctgtgaaaatgctccgagcagatgccaacaagaatg--- 2221

Qy    2317 GCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCA 2376
Db    2222 --------------ccaggaatgattttcttaaggagataaagatcatgtctcggctca 2266
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Qy    2377 AGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATGA 2436
Db    2267 aggacccaaacatcatccatctattatctgtgtgtatcactgatgaccctctctgtatga 2326

Qy    2437 TTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGG 2496
Db    2327 tcactgaatacatggagaatggagatctcaatcagtttctttcccgccacgagcccccta 2386

Qy    2497 ACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGCT 2556
Db    2387 attcttcctccagcg-------------------------atgtacgcactgtcagtt 2419

Qy    2557 ACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCTCCGGCATGCGCTATCTGGCCACAC 2616
Db    2420 acaccaatctgaagtttatggctacccaaattgcctctggcatgaagtacctttcctctc 2479

Qy    2617 TCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACCA 2676
Db    2480 ttaattttgttcaccgagatctggccacacgaaactgtttagtgggtaagaactacacaa 2539

Qy    2677 TCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTGC 2736
Db    2540 tcaagatagctgactttggaatgagcaggaacctgtacagtggtgactattaccggatcc 2599

Qy    2737 AGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGT 2796
Db    2600 agggccgggcagtgctccctatccgctggatgtcttgggagagtatcttgctgggcaagt 2659

Qy    2797 TCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCT 2856
Db    2660 tcactacagcaagtgatgtgtgggcctttggggttactttgtgggagactttcacctttt 2719

Qy    2857 GTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGGTCATCGAGAACGCGGGGGAGT 2916
Db    2720 gtcaagaacagccctattcccagctgtcagatgaacaggttattgagaatactggagagt 2779

Qy    2917 TCTTCCGGGACCAGGGCCGGCAGGTGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGCC 2976
Db    2780 tcttccgagaccaagggaggcagacttacctccctcaaccagccatttgtcctgactctg 2839

Qy    2977 TATATGAGCTGATGCTTCGGTGCTGGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCCC 3036
Db    2840 tgtataagctgatgctcagctgctggagaagagatacgaagaaccgtccctcattccaag 2899

Qy    3037 AGCTGCATCGGTTCCT 3052
Db    2900 aaatccaccttctgct 2915
```

```
RESULT 12
AAV55895
ID   AAV55895 standard; DNA; 3120 BP.
XX
AC   AAV55895;
XX
DT   19-NOV-1998 (first entry)
XX
DE   Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.
XX
KW   PTK; receptor; protein tyrosine kinase; brain tissue; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             485..3049
FT                   /*tag= a
FT                   /product= "PTK subtype tyro-10"
XX
PN   US5811516-A.
XX
PD   22-SEP-1998.
XX
PF   02-JUN-1995;   95US-0456647.
XX
PR   15-MAY-1992;   92US-0884486.
PR   02-MAY-1994;   94US-0237401.
PR   02-JUN-1995;   95US-0456647.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Lai CHC, Lemke GE;
XX
DR   WPI; 1998-530939/45.
DR   P-PSDB; AAW79152.
XX
PT   Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably
PT   expressed in brain tissue
XX
PS   Example 2; Columns 53-60; 46pp; English.
XX
CC   This DNA encodes a novel receptor protein tyrosine kinase (PTK)
CC   polypeptide subtype tyro-10. The invention provides polynucleotide
CC   sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.
CC   The PTK subtypes are found expressed predominantly in the brain tissue.
XX
SQ   Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;
```

```
  Query Match           16.1%;  Score 639.8;  DB 19;  Length 3120;
  Best Local Similarity  56.5%;  Pred. No. 3.4e-130;
  Matches 1552;  Conservative    0;  Mismatches  987;  Indels  210;  Gaps   11;

Qy     348 CTGCTGCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCC 407
Db     509 ctggtgctgctcctgctcttgctcatcctgggttctgcaaaagctcaggttaatccagcc 568

Qy     408 AAGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCT 467
Db     569 atatgccgctatcctctgggcatgtcaggaggccacattccagatgaggacatcacagcc 628

Qy     468 TCCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGG 527
Db     629 tcaagtcagtggtcagaatccacggctgccaaatatgggaggctggactctgaagaagga 688

Qy     528 GATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGA---GGAGGAGTACTTGCAG 584
Db     689 gatggagcctggtgtcctgagattccagtgcaacccgatgacctgaaggaatttctgcag 748

Qy     585 GTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGG 644
Db     749 attgacttgcgaaccctacactttatcactcttgtggggacccaggggcgccatgcaggg 808

Qy     645 GGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGC 704
Db     809 ggtcatggcattgaatttgcacccatgtacaagatcaactacagtcgggatggcagtcgc 868

Qy     705 TGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAG 764
Db     869 tggatctcctggcgtaaccggcatgggaagcaggtgcttgatggaaacagtaacccttat 928

Qy     765 GGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCC 824
Db     929 gatgtattcctgaaggacttggagccacccatcgtcgccagatttgttcgccttatccca 988

Qy     825 CGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGG 884
Db     989 gtcactgaccactccatgaacgtgtgcatgagggttgagctttatggttgtgtctggcta 1048

Qy     885 GATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGG----- 939
Db    1049 gatggcttggtatcctacaatgctccagctggacagcagtttgtactccctggaggctcc 1108

Qy     940 -CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATGGG 998
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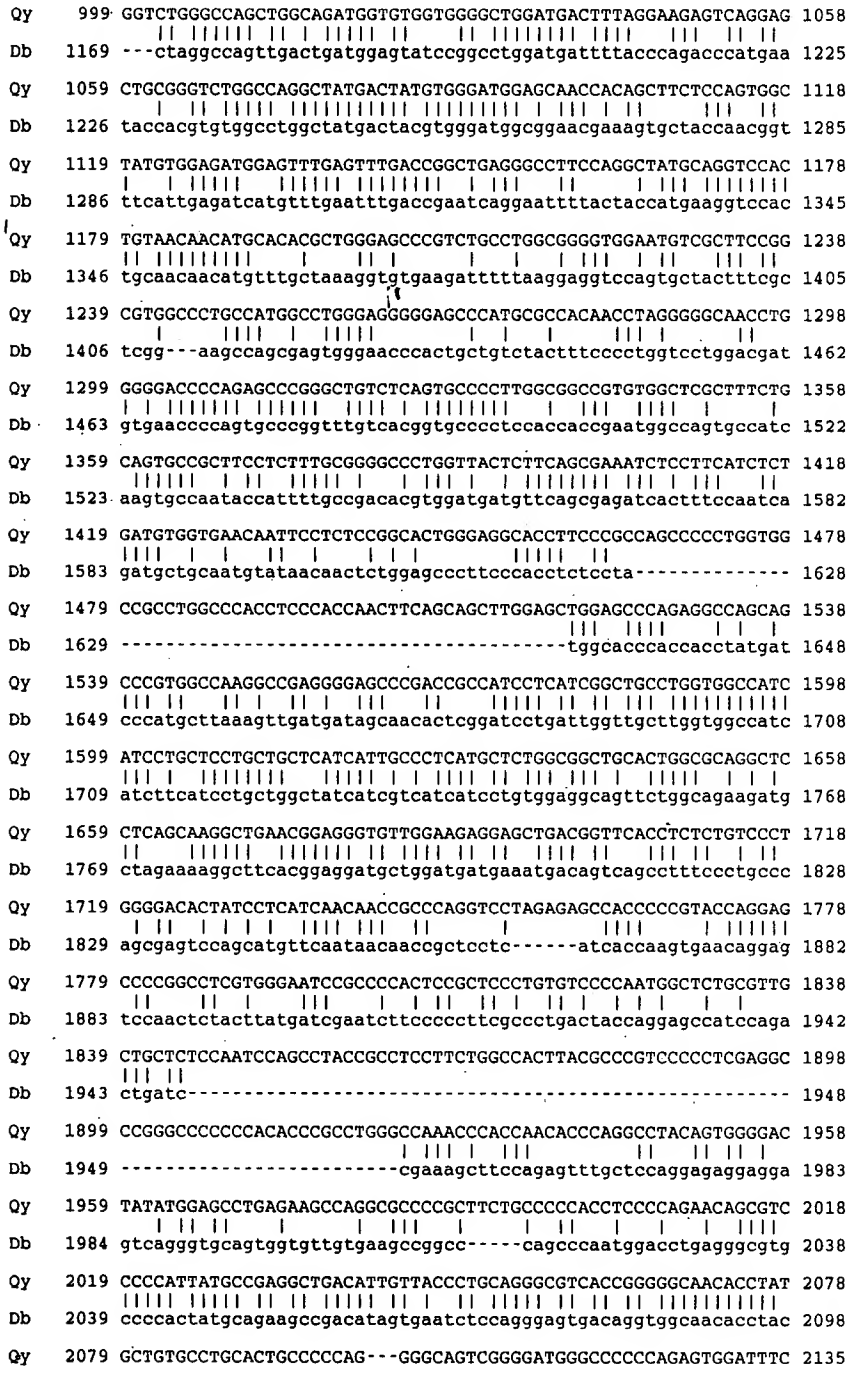

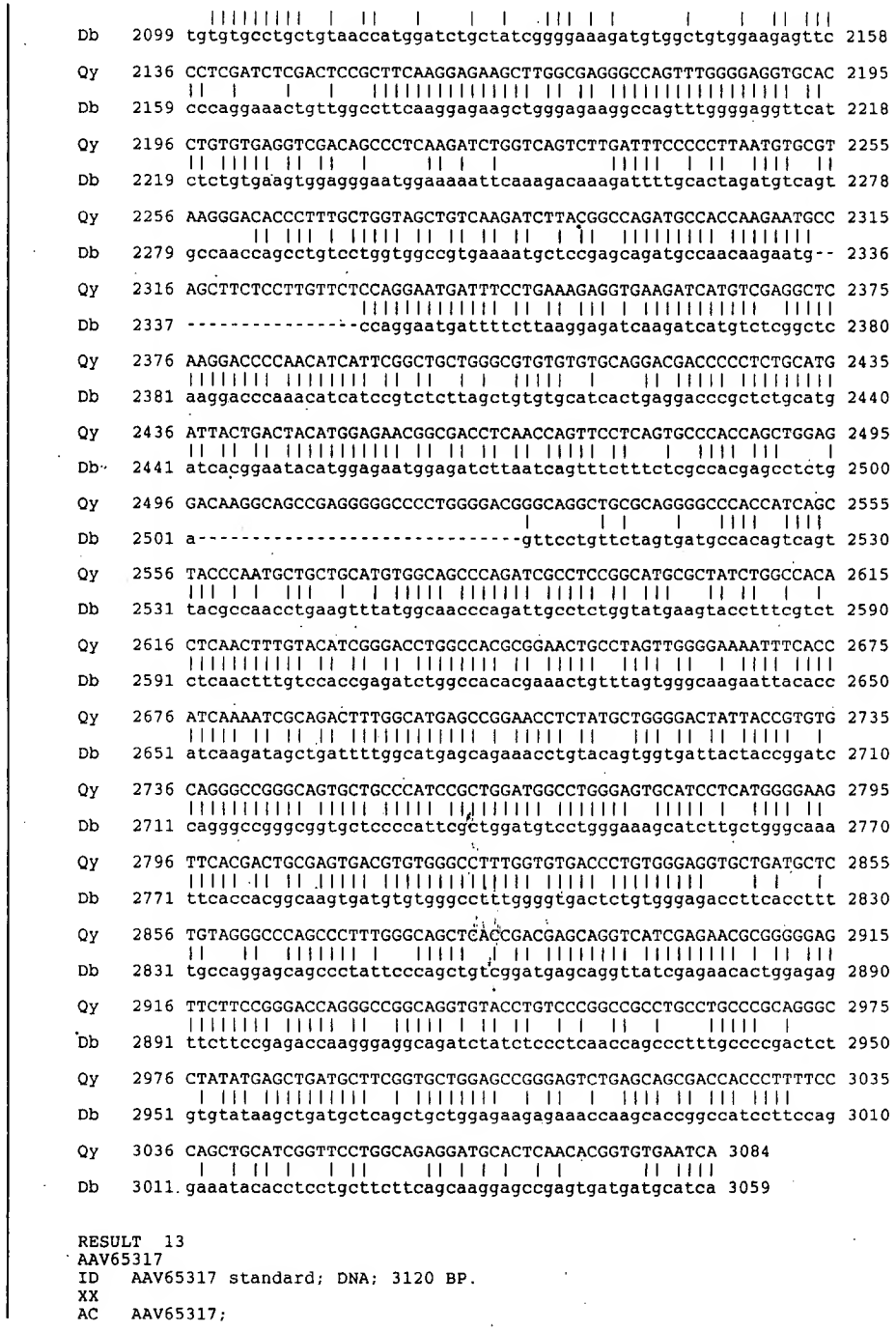

RESULT 13
AAV65317
ID AAV65317 standard; DNA; 3120 BP.
XX
AC AAV65317;

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XX
DT   22-JAN-1999  (first entry)
XX
DE   Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.
XX
KW   PTK; receptor; protein tyrosine kinase; recombinant; grafting;
KW   diagnosis; tumour; skin transplant; connective tissue; tyro-10; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             485..3049
FT                   /*tag= a
FT                   /product= "PTK subtype tyro-10"
XX
PN   US5837448-A.
XX
PD   17-NOV-1998.
XX
PF   02-MAY-1994;    94US-0237401.
XX
PR   15-MAY-1992;    92US-0884486.
PR   02-MAY-1994;    94US-0237401.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Lai CHC,  Lemke GE;
XX
DR   WPI; 1999-023436/02.
DR   P-PSDB; AAW81409.
XX
PT   Nucleic acids encoding protein tyrosine kinase sub:types - for
PT   identification of new sub:types and treatment of diseases associated
PT   with the kinase
XX
PS   Claim 1; Columns 53-58; 47pp; English.
XX
CC   This DNA encodes a receptor protein tyrosine kinase (PTK) subtype
CC   tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
CC   and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
CC   domain and a tissue expression pattern of a receptor PTK subtype selected
CC   from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
CC   tyro-11, and tyro-12, respectively. The polynucleotides are useful for
CC   the detection of tyrosine kinase domain sequences and detection of
CC   tissue expression patterns of PTK subtypes. The cDNAs can also be
CC   injected into oocytes, the protein expressed, and expression products
CC   screened for using antibodies against tyrosine kinase epitopes. These
CC   subtypes sequences can be used for the design of oligonucleotides, for
CC   use in amplification reactions to isolate other subtype sequences. These
CC   detection protocols are used in the diagnosis of diseases associated
CC   with (receptor) PTKs. Recombinant vectors expressing the subtypes can be
CC   used to treat related diseases e.g. tumours, by introduction of the
CC   vectors into skin transplants, then grafting these into the connective
CC   tissue of the dermis, thus specifically targetting tumours as the
CC   proteins are released from the matrix.
XX
SQ   Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;

  Query Match           16.1%;  Score 639.8;  DB 20;  Length 3120;
  Best Local Similarity  56.5%;  Pred. No. 3.4e-130;
  Matches 1552;  Conservative    0;  Mismatches  987;  Indels  210;  Gaps   11;

Qy    348 CTGCTGCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCC 407
Db    509 ctggtgctgctcctgctcttgctcatcctgggttctgcaaaagctcaggttaatccagcc 568

Qy    408 AAGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCT 467
Db    569 atatgccgctatcctctgggcatgtcaggaggccacattccagatgaggacatcacagcc 628

Qy    468 TCCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGG 527
Db    629 tcaagtcagtggtcagaatccacggctgccaaatatgggaggctggactctgaagaagga 688

Qy    528 GATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGA---GGAGGAGTACTTGCAG 584
Db    689 gatggagcctggtgtcctgagattccagtgcaacccgatgacctgaaggaatttctgcag 748

Qy    585 GTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGG 644
Db    749 attgacttgcgaaccctacactttatcactcttgtggggacccaggggcgccatgcaggg 808

Qy    645 GGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGC 704
Db    809 ggtcatggcattgaatttgcacccatgtacaagatcaactacagtcgggatggcagtcgc 868

Qy    705 TGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAG 764
Db    869 tggatctcctggcgtaaccggcatgggaagcaggtgcttgatggaaacagtaacccttat 928

Qy    765 GGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTACCCC 824
Db    929 gatgtattcctgaaggacttggagccacccatcgtcgccagatttgttcgccttatccca 988

Qy    825 CGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGG 884
Db    989 gtcactgaccactccatgaacgtgtgcatgagggttgagctttatggttgtgtctggcta 1048

Qy    885 GATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGG----- 939
Db   1049 gatggcttggtatcctacaatgctccagctggacagcagtttgtactccctggaggctcc 1108

Qy    940 -CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATGGG 998
Db   1109 atcatttatctgaatgattctgtctatgatggagctgttgggtacagcatgactgaaggg 1168

Qy    999 GGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAG 1058
Db   1169 ---ctaggccagttgactgatggagtatccggcctggatgattttacccagacccatgaa 1225

Qy   1059 CTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGC 1118
Db   1226 taccacgtgtggcctggctatgactacgtgggatggcggaacgaaagtgctaccaacggt 1285

Qy   1119 TATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCAC 1178
Db   1286 ttcattgagatcatgtttgaatttgaccgaatcaggaattttactaccatgaaggtccac 1345

Qy   1179 TGTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGG 1238
Db   1346 tgcaacaacatgtttgctaaaggtgtgaagatttttaaggaggtccagtgctactttcgc 1405

Qy   1239 CGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTG 1298
Db   1406 tcgg---aagccagcgagtgggaacccactgctgtctactttccccctggtcctggacgat 1462

Qy   1299 GGGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTG 1358
Db   1463 gtgaaccccagtgcccggtttgtcacggtgcccctccaccaccgaatggccagtgccatc 1522

Qy   1359 CAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCT 1418
Db   1523 aagtgccaataccattttgccgacacgtggatgatgttcagcgagatcactttccaatca 1582

Qy   1419 GATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGG 1478
Db   1583 gatgctgcaatgtataacaactctggagcccttcccacctctccta-------------- 1628

Qy   1479 CCGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAG 1538
Db   1629 ----------------------------------------tggcacccaccacctatgat 1648

Qy   1539 CCCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATC 1598
Db   1649 cccatgcttaaagttgatgatagcaacactcggatcctgattggttgcttggtggccatc 1708
```

```
Qy   1599 ATCCTGCTCCTGCTGCTCATCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTC 1658
Db   1709 atcttcatcctgctggctatcatcgtcatcatcctgtggaggcagttctggcagaagatg 1768

Qy   1659 CTCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCT 1718
Db   1769 ctagaaaaggcttcacggaggatgctggatgatgaaatgacagtcagcctttccctgccc 1828

Qy   1719 GGGGACACTATCCTCATCAACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAG 1778
Db   1829 agcgagtccagcatgttcaataacaaccgctcctc------atcaccaagtgaacaggag 1882

Qy   1779 CCCCGGCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTG 1838
Db   1883 tccaactctacttatgatcgaatcttccccctccgccctgactaccaggagccatccaga 1942

Qy   1839 CTGCTCTCCAATCCAGCCTACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGC 1898
Db   1943 ctgatc---------------------------------------------------- 1948

Qy   1899 CCGGGCCCCCCCCACACCCGCCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGGGAC 1958
Db   1949 -------------------------cgaaagcttccagagtttgctccaggagaggagga 1983

Qy   1959 TATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTC 2018
Db   1984 gtcagggtgcagtggtgttgtgaagccggcc-----cagcccaatggacctgagggcgtg 2038

Qy   2019 CCCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTAT 2078
Db   2039 ccccactatgcagaagccgacatagtgaatctccagggagtgacaggtggcaacacctac 2098

Qy   2079 GCTGTGCCTGCACTGCCCCCAG---GGGCAGTCGGGGATGGGCCCCCCAGAGTGGATTTC 2135
Db   2099 tgtgtgcctgctgtaaccatggatctgctatcggggaaagatgtggctgtggaagagttc 2158

Qy   2136 CCTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCAC 2195
Db   2159 cccaggaaactgttggccttcaaggagaagctgggagaaggccagtttggggaggttcat 2218

Qy   2196 CTGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGT 2255
Db   2219 ctctgtgaagtggagggaatggaaaaattcaaagacaaagattttgcactagatgtcagt 2278

Qy   2256 AAGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTACGGCCAGATGCCACCAAGAATGCC 2315
Db   2279 gccaaccagcctgtcctggtggccgtgaaaatgctccgagcagatgccaacaagaatg-- 2336

Qy   2316 AGCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTC 2375
Db   2337 ----------------ccaggaatgattttcttaaggagatcaagatcatgtctcggctc 2380

Qy   2376 AAGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTGTGCAGGACGACCCCCTCTGCATG 2435
Db   2381 aaggacccaaacatcatccgtctcttagctgtgtgcatcactgaggacccgctctgcatg 2440

Qy   2436 ATTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAG 2495
Db   2441 atcacggaatacatggagaatggagatcttaatcagtttctttctcgccacgagcctctg 2500

Qy   2496 GACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTGCGCAGGGGCCCACCATCAGC 2555
Db   2501 a------------------------------gttcctgttctagtgatgccacagtcagt 2530

Qy   2556 TACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCTCCGGCATGCGCTATCTGGCCACA 2615
Db   2531 tacgccaacctgaagtttatggcaacccagattgcctctggtatgaagtacctttcgtct 2590

Qy   2616 CTCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAAAATTTCACC 2675
Db   2591 ctcaactttgtccaccgagatctggccacacgaaactgtttagtgggcaagaattacacc 2650

Qy   2676 ATCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTATTACCGTGTG 2735
Db   2651 atcaagatagctgattttggcatgagcagaaacctgtacagtggtgattactaccggatc 2710

Qy   2736 CAGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAG 2795
Db   2711 cagggccgggcggtgctccccattcgctggatgtcctgggaaagcatcttgctgggcaaa 2770

Qy   2796 TTCACGACTGCGAGTGACGTGTGGGCCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTC 2855
Db   2771 ttcaccacggcaagtgatgtgtgggcctttggggtgactctgtgggagaccttcaccttt 2830

Qy   2856 TGTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGGTCATCGAGAACGCGGGGGAG 2915
Db   2831 tgccaggagcagccctattcccagctgtcggatgagcaggttatcgagaacactggagag 2890

Qy   2916 TTCTTCCGGGACCAGGGCCGGCAGGTGTACCTGTCCCGGCCGCCTGCCTGCCCGCAGGGC 2975
Db   2891 ttcttccgagaccaagggaggcagatctatctccctcaaccagccctttgcccgactct 2950

Qy   2976 CTATATGAGCTGATGCTTCGGTGCTGGAGCCGGGAGTCTGAGCAGCGACCACCCTTTTCC 3035
Db   2951 gtgtataagctgatgctcagctgctggagaagagaaaccaagcaccggccatccttccag 3010

Qy   3036 CAGCTGCATCGGTTCCTGGCAGAGGATGCACTCAACACGGTGTGAATCA 3084
Db   3011 gaaatacacctcctgcttcttcagcaaggagccgagtgatgatgcatca 3059
```

RESULT 14
AAH99505
ID AAH99505 standard; cDNA; 2725 BP.
XX
AC AAH99505;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein encoding cDNA sequence SEQ ID NO:340.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US35017.
XX
PR 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457603/49.
DR P-PSDB; AAM25564.

XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
PS Claim 1; Page 452-453; 1217pp; English.
XX
CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production, The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 2725 BP; 678 A; 700 C; 664 G; 683 T; 0 other;

Query Match 13.7%; Score 544.2; DB 22; Length 2725;
Best Local Similarity 56.2%; Pred. No. 2.7e-109;
Matches 1372; Conservative 0; Mismatches 858; Indels 213; Gaps 10;

```
Qy    405 GCCAAGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCT 464
Db      8 gctatatgccgctatcctctgggcatgtcaggaggccagattccagatgaggacatcaca 67

Qy    465 GCTTCCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGAC 524
Db     68 gcttccagtcagtggtcagagtccacagctgccaaatatggaaggctggactcagaagaa 127

Qy    525 GGGGATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGA---GGAGGAGTACTTG 581
Db    128 ggggatggagcctggtgccctgagattccagtggaacctgatgacctgaaggagtttctg 187

Qy    582 CAGGTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCC 641
Db    188 cagattgacttgcacaccctccattttatcactctggtggggacccaggggcgccatgca 247

Qy    642 GGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGC 701
Db    248 ggaggtcatggcatcgagtttgcccccatgtacaagatcaattacagtcgggatggcact 307

Qy    702 CGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCT 761
Db    308 cgctggatctcttggcggaaccgtcatgggaaacaggtgctggatggaaatagtaacccc 367

Qy    762 GAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCGCTTCTAC 821
Db    368 tatgacattttcctaaaggacttggagccgcccattgtagccagatttgtccggttcatt 427

Qy    822 CCCCGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCCTCTGG 881
Db    428 ccagtcaccgaccactccatgaatgtgtgtatgagagtggagctttacggctgtgtctgg 487

Qy    882 AGGGATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATCTGAGG-- 939
Db    488 ctagatggcttggtgtcttacaatgctccagctgggcagcagtttgtactccctggaggt 547

Qy    940 ----CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTAT 995
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Db    548 tccatcatttatctgaatgattctgtctatgatggagctgttggatacagcatgacagaa 607

Qy    996 GGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAG 1055
Db    608 ggg---ctaggccaattgaccgatggtgtgtctggcctggacgatttcacccagacccat 664

Qy   1056 GAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCTCCAGT 1115
Db    665 gaataccacgtgtggcccggctatgactatgtgggctggcggaacgagagtgccaccaat 724

Qy   1116 GGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTC 1175
Db    725 ggctacattgagatcatgtttgaatttgaccgcatcaggaatttcactaccatgaaggtc 784

Qy   1176 CACTGTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTC 1235
Db    785 cactgcaacaacatgtttgctaaaggtgtgaagatctttaaggaggtacagtgctacttc 844

Qy   1236 CGGCGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGGGCAAC 1295
Db    845 cgctctgaa---gccagtgagtgggaacctaatgccatttccttccccttgtcctggat 901

Qy   1296 CTGGGGGACCCCAGAGCCCGGGCTGTCTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTT 1355
Db    902 gacgtcaaccccagtgctcggtttgtcacggtgcctctccaccaccgaatggccagtgcc 961

Qy   1356 CTGCAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATC 1415
Db    962 atcaagtgtcaatacctattttgcagatacctggatgatgttcagtgagatcaccttccaa 1021

Qy   1416 TCTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGG 1475
Db   1022 tcagatgctgcaatgtacaacaactctgaagccctgcccacctctccta---------- 1070

Qy   1476 TGGCCGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAG 1535
Db   1071 ----------------------------------------tggcacccacaacctat 1087

Qy   1536 CAGCCCGTGGCCAAGGCCGAGGGGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCC 1595
Db   1088 gatccaatgcttaaagttgatgacagcaacactcggatcctgattggctgcttggtggcc 1147

Qy   1596 ATCATCCTGCTCCTGCTGCTCATCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGG 1655
Db   1148 atcatctttatcctcctggccatcattgtcatcatcctctggaggcagttctggcagaaa 1207

Qy   1656 CTCCTCAGCAAGGCTGAACGGAGGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTC 1715
Db   1208 atgctggagaaggctttctcggaggatgctggatgatgaaatgacagtcagcctttccctg 1267

Qy   1716 CCTGGGGACACTATCCTCATCAACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAG 1775
Db   1268 ccaagtgattctagcatgttcaacaa----------------------------taaccgc 1300

Qy   1776 GAGCCCCGGCCTCGTGGGAATCCGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCG 1835
Db   1301 tcctcatcacctagtgaacaagggtccaactcgacttacgatcgcatcttt--------- 1351

Qy   1836 TTGCTGCTCTCCAATCCAGCCTACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGA 1895
Db   1352 ----------------------------------------------------ccccctt 1357

Qy   1896 GGCCCGGGCCCCCCCACACCCGCCTGGGCCAAACCCACCAACACCCAGGCCTACAGTGGG 1955
Db   1358 cgccctgactaccaggagccatccaggctgatacgaaaactcccagaatttgctccaggg 1417

Qy   1956 GACTATATGGAGCCTGAGAAGCCAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGC 2015
Db   1418 gaggaggagtcaggctgcagcggtgttgtgaagccagtccagcccagtggccctgagggg 1477

Qy   2016 GTCCCCCATTATGCCGAGGCTGACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACC 2075
Db   1478 gtgccccactatgcagaggctgacatagtgaacctccaaggagtgacaggaggcaacaca 1537
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Qy   2076 TATGCTGTGCCTGCACTGCCCCCAGGGGCAGTCGGGGA---------TGGGCCCCCCAGA 2126
          ||  | ||||||||  |  ||   |      ||   |          |||       ||
Db   1538 tactcagtgcctgccgtcaccatggacctgctctcagggaaaagatgtggctgtgggagg 1597

Qy   2127 GTGGATTTCCCTCGATCTCGACTCCGCTTCAAGGAGAAGCTTGGCGAGGGCCAGTTTGGG 2186
          | |  |  |||  |    |  ||    ||||| |||||||| || || || |||||||||
Db   1598 gagtttcccccagggaaactcctaactttcaaagagaagctgggagaaggacagtttgggg 1657

Qy   2187 GAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTGATTTCCCCCTT 2246
          |||||  || || |||||  || ||  |     || |  |          |||||  ||||
Db   1658 gaggttcatctctgtgaagtggagggaatggaaaaattcaaagacaaagattttgccctа 1717

Qy   2247 AATGTGCGTAAGGGACACCCTTTGCTGGTAGCTGTCAAGATCTTACGGCCAGATGCCACC 2306
           ||||  ||      || ||| | ||||| ||||| || ||  | ||  ||||||||| |
Db   1718 gatgtcagtgccaaccagcctgtcttggtggctgtgaaaatgctccgagcagatgccaac 1777

Qy   2307 AAGAATGCCAGCTTCTCCTTGTTCTCCAGGAATGATTTCCTGAAAGAGGTGAAGATCATG 2366
          |||||||                ||||||||||||| || || ||| | |||||||||
Db   1778 aagaatg-----------------ccaggaatgattttcttaaggagataaagatcatg 1819

Qy   2367 TCGAGGCTCAAGGACCCCAACATCATTCGGCTGCTGGGCGTGTGTGTGCAGGACGACCCC 2426
          ||  ||||||||||||| |||||||| |  ||  |    ||||||  |    || |||||
Db   1820 tctcggctcaaggacccaaacatcatccatctattatctgtgtgtatcactgatgaccct 1879

Qy   2427 CTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCCTCAGTGCCCAC 2486
          |||||  |||||  |||||  |||||||||||  || || |||||  |||||  ||      ||||
Db   1880 ctctgtatgatcactgaatacatggagaatggagatctcaatcagtttctttcccgccac 1939

Qy   2487 CAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTGCGCAGGGGCCC 2546
          ·|||      |     |  ||   |                                 | |  | |
Db   1940 gagccccctaattcttcctccagcg---------------------------atgtacgc 1972

Qy   2547 ACCATCAGCTACCCAATGCTGCTGCATGTGGCAGCCCAGATCGCCTCCGGCATGCGCTAT 2606
          ||  |||| ||| | |  |||  |  | ||||  |||| || |||||  ||||||    ||
Db   1973 actgtcagttacaccaatctgaagtttatggctacccaaattgcctctggcatgaagtac 2032

Qy   2607 CTGGCCACACTCAACTTTGTACATCGGGACCTGGCCACGCGGAACTGCCTAGTTGGGGAA 2666
          ||  || | || ||  ||||| || || || |||||||| || |||||  |||| ||  |
Db   2033 ctttcctctcttaattttgttcaccgagatctggccacacgaaactgtttagtgggtaag 2092

Qy   2667 AATTTCACCATCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATGCTGGGGACTAT 2726
          || | ||| ||||| || || |||||||| |||||| |||||||  ||   ||| ||||||
Db   2093 aactacacaatcaagatagctgactttggaatgagcaggaacctgtacagtggtgactat 2152

Qy   2727 TACCGTGTGCAGGGCCGGGCAGTGCTGCCCATCCGCTGGATGGCCTGGGAGTGCATCCTC 2786
          |||||  | ||||||||||||||||| || ||||||||||| | |||||| | ||| |
Db   2153 taccggatccagggccgggcagtgctccctatccgctggatgtcttgggagagtatcttg 2212

Qy   2787 ATGGGGAAGTTCACGACTGCGAGTGACGTGTGGGCCTTTGGTG 2829
          |||| ||||||||  || || |||||  |||||||||||||| |
Db   2213 ctgggcaagttcactacagcaagtgatgtgtgggcctttgggg 2255
```

RESULT 15
AAS57829/c
ID AAS57829 standard; cDNA; 563 BP.
XX
AC AAS57829;
XX
DT 13-FEB-2002 (first entry)
XX
DE cDNA #505 encoding portion of a human colon tumour protein.
XX
KW Human; colon tumour protein; colon cancer; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200173027-A2.
XX
PD 04-OCT-2001.
XX
PF 22-MAR-2001; 2001WO-US09246.
XX
PR 24-MAR-2000; 2000US-191597P.
PR 04-MAY-2000; 2000US-202024P.
PR 05-MAY-2000; 2000US-202189P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Meagher MJ, Xu J, King GE;
XX
DR WPI; 2001-611627/70.
XX
PT New colon tumour proteins and related nucleic acid, useful for
PT treatment, prevention, diagnosis and monitoring of cancer -
XX
PS Claim 4; Page 138; 299pp; English.
XX
CC Th present invention relates to the isolation of novel cDNA sequences
CC encoding for at least an immunogenic portion of human colon tumour
CC proteins. The sequences of the invention are useful in pharmaceutical
CC compositions and vaccines for the prevention and treatment of cancers
CC such as colon cancer. They are also useful for the diagnosis and
CC monitoring of such cancers. Antibodies to the colon tumour proteins
CC and antigen presenting cells that express polynucleotides encoding
CC colon tumour proteins can be used to inhibit the development of
CC cancers. T-cells that react specifically with colon tumour proteins
CC are useful for removing tumour cells from samples (e.g. blood) and
CC for cancer treatment. The polynucleotides sequences are also useful in
CC gene therapy. AAS57325-AAS58880 represent the cDNA sequences of the
CC invention that encode for portions of human colon tumour proteins.
XX
SQ Sequence 563 BP; 116 A; 207 C; 139 G; 97 T; 4 other;

Query Match 13.2%; Score 522.8; DB 23; Length 563;
Best Local Similarity 97.7%; Pred. No. 8e-105;
Matches 549; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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Qy    511 TGGAGAGCAGTGACGGGGATGGGGCC-TGGTGCCCCGCAGGGTCGGTGTTTCCC-AAGGA 568
          || | | |||| ||||| |||||||| |||| |||||||||||||||||||||| |||||
Db    562 TGAAAANCAGTAACGGGAATGGGGCCTTGGTNCCCCGCAGGGTCGGTGTTTCCCAAAGGA 503

Qy    569 GGAGGAGTACTTGCAGGTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCA 628
          | |||||||||||||||||||||||||||||| |||||||||| | ||||||||||||
Db    502 GNAGGAGTACTTGCAGGTGGATCTACAACGACTGCACCTGGTGGNTTTGGTGGGCACCCA 443

Qy    629 GGGACGGCATGCCGGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTC 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 GGGACGGCATGCCGGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTC 383

Qy    689 CCGGGATGGTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGG 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 CCGGGATGGTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGG 323

Qy    749 CAATGAGGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACT 808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 CAATGAGGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACT 263

Qy    809 GGTTCGCTTCTACCCCCGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTA 868
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    262 GGTTCGCTTCTACCCCCGGGCTGACCGGGTCATGAGCGTCTGTCTGCGGGTAGAGCTCTA 203

Qy    869 TGGCTGCCTCTGGAGGGATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTA 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 TGGCTGCCTCTGGAGGGATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTA 143

Qy    929 TTTATCTGAGGCCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 TTTATCTGAGGCCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACT 83

Qy    989 GCAGTATGGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 GCAGTATGGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAA 23
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Qy    1049 GAGTCAGGAGCTGCGGGTCTGG 1070
           ||||||||||||||||||||||
Db      22 GAGTCAGGAGCTGCGGGTCTGG 1
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Search completed: October 5, 2002, 20:29:15
Job time: 19933 sec